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C       28       38.2       1.4       8561       3       US-09-112-450-3       Sequence 3, Appli         C       29       38.2       1.4       8561       4       US-09-191-211-10       Sequence 3, Appli         30       38.2       1.4       9844       4       US-09-191-211-10       Sequence 10, Appl         30       38.2       1.4       9844       4       US-09-191-211-10       Sequence 10, Appl         31       38       1.4       2007       2       US-08-743-637B-169       Sequence 169, App         33       38       1.4       2007       3       US-08-914-01169       Sequence 169, App         33       38       1.4       2007       3       US-08-940B-169       Sequence 1710, App         33       38       1.4       2007       3       US-08-940B-169       Sequence 1710, App         33       37.8       1.4       4140       3       US-08-944-731-2       Sequence 1710, App         34       37.8       1.4       4920       3       US-08-946-855A-1       Sequence 1710, App         35       37.8       1.4       8920       2       US-08-946-855A-1       Sequence 17, App         37       37.8	38 37.8 1.4 1645976 4 US-09-632-570-1 39 37.4 1.4 2663 1 US-08-166-7438-3 41 37.4 1.4 2663 1 US-08-166-7438-3 41 37.4 1.4 76962 4 US-09-206-763-553-3 42 37.2 1.4 942 4 US-09-270-767-19049 43 37.2 1.4 942 4 US-09-270-767-19049 44 37.2 1.4 1928 4 US-09-674-826B-5 45 36.8 1.3 80246 3 US-09-078-294-4	RESULT 1 US-09-232-160-3 Sequence 3, Application US/09232160 Patent No. 6368794 GENERAL INPORMATION:	A PFULCANT: STEEVE DATHEL APPLICANT: STEEVE DATHEL APPLICANT: SUSAN G. StUART APPLICANT: SUSAN G. StUART APPLICANT: LAURA StUVE TITLE OF INVENTION: DETERTION OF ALTERED EXPRESSION OF GENES REGULATING CELL TITLE OF INVENTION: DETERTION FILE REFERENCE: PA-0003 US CURRENT APPLICATION NUMBER: US/09/232,160 CURRENT FILING DATE: 1999-01.15 CURRENT FILING DATE: 1999-01.15	NUMBER OF SEQ ID NOS: 23 SOFTWARE: PERL Program SEQ ID NO 3 LENGTH: 1853	; TYPE: DNA ; CRCANISM: Homo sapiens ; FEATURE: - INPORMATION: 1283330 11S-09-272-160-3	N NANANANANANANANANANANANANANANANANANAN
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: November 29, 2004, 08:42:07 ; Search time 227 Seconds Run on: November 29, 2004, 08:42:07 / Search time 227 Seconds	: US-09-989-920-100 ct score: 2754 nce: 1 gccagaagcagcctcagctta. ng table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 hed: 824507 segs, 355394441 residues	Total number of Alts satisfying chosen parameters: 1643014 Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<pre>Database : Issued Patents NA:* 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:* 2: /cgn2_6/ptodata/1/ina/6A_COMB.seq:* 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:* 4: /cgn2_6/ptodata/1/ina/6A_COMB.seq:* 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* 6: /cgn2_6/ptodata/1/ina/Packfiles1.seq:*</pre>	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	summaries Query Match Length DB ID	1       1747.6       63.5       1853       3       US-09-232-160-3       Sequence 3, Appli         2       1.9       6310       3       US-09-880-427-2       Sequence 14, Appl         4       49       1.8       6330       3       US-09-306-538F-2       Sequence 2, Appli         5       49       1.8       19806       4       US-09-706-538F-2       Sequence 3, Appli         5       49       1.8       19806       4       US-09-718-037-3       Sequence 3, Appli         6       49       1.8       19806       4       US-09-718-037-3       Sequence 3, Appli         6       49       1.8       19806       4       US-09-718-037-3       Sequence 3, Appli         7       47       1.7       265       4       US-09-713-0986-1       Sequence 12.137, A         7       41.4       1.5       2104       4       US-09-713-0996-23077       Sequence 12.137, A         7       1.1       1.5       3294       4       US-09-713-0996-11322       Sequence 12.137, A         7       1.1       1.5       3144       US-09-713-0996-11322       Sequence 12.137, A         7       1.4       1.5       1141       US-09-713-0996-113223

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CCTAGTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAGCCTCTTCCCA 1713 TGTGTCCAGCTGCTTCCTGCTACAAAGGGGGACTGCTCACAGTGGCCTCAGCTTGGTGG 1773 961 CACTCCAGGGGCAGACAGCAGCCACTCCTTCCTTCCTCGTGAGTAACAGTAGTGGTAA 1020 1021 GCAGCTGGGGGCTAACAGGCTAGGCTTGTGTGTCTGGGCATTTGGTCAGGCTTCTCACTCGA 1080 CTTTCCTTCTTGCCGCCTGCTTCCTGGGGGACCCGCTGGGCCTTTGGTCTGCATC 1533 CCCTGGCCAGGTCCCTCAGGGTTGATGCGTGGAGGAGGACTTTGAGCAGTGGGGGGGCAGC 1593 301 ATGACTTGGTTTGCGCTTGGAGGGGGGGGGGGGGGGGGTTTCGGGGGGGTTTCTGCGTTAAC 360 421 TGCTTCAGCTGCTGCAGAGTCCACCCCGCCCTCGTGGGGAATGCAGAGGCCCTTTG 1081 TCCTCCTAAAGCAATGGGGGGGGCCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGGG 1321 AGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGGAAGGGGACTGTTGGGGGGCCTC 361 cercentaricaccentercerentercerentercereceaccecenteragericac TGCTTCAGCTGGCTGCTGCAGAGTCCACCCCGGCCTCGTGGTGGGGAATGCAGAGCCCTTTG AGTGGCCTCCTGGCCAGCTCACACTCTTGTCCTGGGAGGGGGCAGCCTGATCTCACCTCCA CTAGTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAGCCTCTTCCCA TGTGTCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGG TTTTGAGGGGCCGCCCCCGGGCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATC TTTTGAGGGCCCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATC 1894 CCGGCTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCCTGGTGTCTT CGGCTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCCGGGGTGTCTT TCCTCCCTAAAGCAATGGGGGGGCCCCCACTAGCCCCAGTTTTCAGGAAGTCAACTGGGAG GTTAGATGGGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGGCTAGGTTGAGCTTCCTGG GTTAGATGGGGGCCAGGGTCCCACAGCTACTGATGGCCCGGGGGCTTGAGGCTTCCTGG TETCCAGTCCGGATCCTCCATGCTCTCCAGATAGGTGGGACAAGTTCTTT 1201 TGTCCAGTCCCGGATCCCACTTGCATCTCATGCTCCAGATAGGTGGGGACAAGTTCTTT 1261 rercacastiscredecticrercereadescercartiscredectedererecrescada AAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGGGGACTGTTTGGGGGTGCCTC TCTGCAGCCTCCCCGTGCTGCTGGTGGAGCAGGTTACTGTGTCTCTCAATGTTCATGTAT TGCCATTGGAGGATGGACGACCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGT 2014 GCAGCTGGGGCTAACAGGCTAGGCTTTGTGTTCTGCGCGCATTTGGTCAGCTTCTCACTCGA correctinancacecarcitererererereecteececcecetreeaageri 1474 1594 661 -1774 781 1354 1414 1534 1654 1714 2134 1141 2194 2254 2314 1834 1954 2074 721 106 go q g Q qq 20 Con 10 qo 8 qq 8 ð Ş q DD. ĝ â ą g đ ð à 8 9 8 a ð 8 -00 9 <u>o</u> 8 ୍ବି 8

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	2434 TTAAAATGATTTTTTTTTAAGGATGTAACCTCCACACTTTTTTCCCGGATTGGGTGACTCT 2 	2494 TTTCTAAAGGTGGTGGGGGGGTTCGTCGGGGGTGGGTGGG	2554 TGTGAGAGGTCCTGGGGAGGGGGGGGGTTGAGCTCAAGGTTGTCCTACTGCCATGTTTTTG 2 	2614 TACCTGAAATAAAGCATATTTTGCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTG 2 	2674 TATGTGGGGATCTGGGTTGGGTTAGATGCAAATAAAACTCACATTGFAAGAAAAAAAA 2 	2734 AAAAAAAAAAAAAA 2747               1741 AAAACAAAAGAGA 1754	<pre>SULT 2 -00-232-463-14 Sequence 14, hpplication US/08232463 Fatent No. 5670367 GENERAL INFORMATION: APPLICANT: SCHERINGER, F. APPLICANT: SCHERINGER, F. APPLICANT: SCHERINGER, F.G. APPLICANT: SCHERING, RECOMBINANT FOWLPOX VIRUS NUMMER OF SEQUENCES: 52 ADDRESSEE: F0-10-4 &amp; Lardner S CARESPONDENCE ADDRESS: CARESPONDENCE ADDRESS: ADDRESSEE: F0-10-4 &amp; Lardner S CONTY: AL-ARANTIA STATE: VA CONTY: USA CONTY: USA CONTY</pre>
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I	<u> </u>	5 1	<u>с</u> 1	<u>о</u> ц	0 D	<u>о</u> ц	Mail Proc. 2010. The rest of the test of test of the test of the test of test o

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TELEX: 899149 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single

TOPOLOGY: linear IMMEDIATE SOURCE: CLONE: pTZgpt-F1s

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Matches 91; Conservative 0; Mismatches 70; Indels 0; Gaps 0;	QY 1061 TACTCAATTATTGTATTTTGGATTTTAGAATTTGTGGGAAATTGTTG	Qy     1121     TACGCCAACATATATGATTTGCCTCTTGGCCTGAAAATATTTACCGTCT     1180       Qy     1121     111     111     111     111     111     111       Db     4774     TACCTGATAATATTCATTATTTTGCCTGCCTGGCCTGGC	QY 1181 AGCCGGTTACAGAAAAAGTCTGGTGACTAGGCCAGAGCC 1221 	RESULT 4 US-09-306-538B-2 	; Patent No. 6372463 ; GENERAL INFORMATION: ; APPLICANT Simon Andrag	us P. Juji	n NULTEL AND AND ALCOURS AND AND ASS. The Mutated Proteins, and Uses 09/306,538B	CURRENT FILING DATE: 1999-05-05 NUMBER OF SEQ ID NOS: 5 SEQ ID NO 2 LENGTH: 6330	TIVE: DNA CREATINE: Homo sapiens FEATURE: NAME/KEY: unsure		Query Match 1.8%; Score 49; DB 3; Length 6330; Best Local Similarity 56.5%; Pred. No. 0.0013; Matches 91; Conservative 0; Mismatches 70; Indels 0; Gaps 0;	QY       1061       TACTCAATTATTGAATTTAAAAAATTGTGGAAATTTGTTGCTCT       1120         D	QY       1121       TACGCCAACATATATATTGATTTGCCTCTTGGCTCTGAAAGCCCAAATATTTACCGTCT       1180         D       111	1181 4834	RESULT 5 TIC-AG-TAAA-APA-3	одо	APPLICANT: GONG, FANGcheng et al TITLE OF INVENTION: ISOLATED HUMAN DEHYDROGENASES, NUCLEIC TITLE OF INVENTION: ACLO MOLECULES ENCODING THESE HUMAN DEHYDROGENASES, AND USES	FILE DEFERENCE: CLOOIDS FILE REFERENCE: CLOOIDS CURRENT APPLICATION NUMBER: US/09/740,028A ; CURRENT FILING DATE: 2000-12-20 ; MINNENT OF GED TO NOC.	SOFTMARE: FastSEQ for Windows Version 4.0 5 SOFTMARE: FastSEQ for Windows Version 4.0
US - 08 - 232 - 463 - 14	Query Match 1.9%; Score 52; DB 1; Length 7218; Best Local Similarity 12.2%; Pred. No. 0.00018; Matches 61; Conservative 213; Mismatches 228; Indels 0; Gaps 0;	Qy     1276     CTTTTTTAAAGAATAAAATGACTTGGTTTGGCTTGGAAGCAGGGGAAGCATTCAGATG     1335       Db     1005     CGTTTGCCATACGCTCACCAGAATTAATTCCGAGGCTGCAGGGAGGCAGCTTGCG     1064	QY 1336 AGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCGTGGGCGAGCC 1395   : :::: : :::::::::::::::::::::::::::	QY 1396 CCCTTTGGAAGGTTCTGGTGCTTCAGCTGCTGCAGAGTCCACCCGCGTGGTG 1455 11111 1111 1111 111111111111111111	Qy         1456         GGAATGCAGAGCCTTTGCTTTCTTTTTTTTTTTTCTGGTACCGGCT         1515           Db         1456         111111111111111111111111111111111111	QY 1516 GGGCCTTTGGTCTCCCTGGCCAGGCTCCTCAGGGTTGATGCGTGGAGAAGAACTT 1575 1111111111111111111111111111111111	QY 1576 TGAGCAGTGGCAGCAGCAGCAGCCAGCCAGCCACACACTCTTGTCCTGGGAGGGGC 1635 i i i i i i i i i i i i i i i i i i i	Oy         1636         AGCCTGATCTCACCTAGTACCTTGGGGACTGAGGACTTTTGGCTTCTCGGAG         1695           11         11         111         111         1495           Db         1365         YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	Oy     1696     CCTGCAAGCCTCTTCCCAGGTGCTGGCTGCTACAAGGGGGCTGCTCACA     1755       Db     1425     YYYYYYYYYYYYYYCTATCTTCTTTATCTTTACTAGTTAGGTAGGTAATTACA     1484	QY 1756 GTGGCCTCAGCTTGGTGGTTTT 1777 1.105 GTGGCCTCAGCTTGGTGGTTTT 1777 1.105 GTGCTCTGGTGTTTTT 1505	TILLS 3	US-09-880-427-2 ; sequence 2, Application US/09880427 ; Patent No. 6358728 ; GENERAL INFORMATION:	APPLICANT: Simon, Andras APPLICANT: Briksson, Ulf APPLICANT: Dryia, Thaddeus P.	APPLICANT: Yanamoto, Hoyuji TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof FILR REFERENCE: LUD 5601	; CURRENT APPLICATION NUMBER: US/09/880,427 ; CURRENT FILING DATE: 2001-06-13 ; PRIOR APPLICATION NUMBER: US 09/306,538	FKLOK FILING DATE: 1999-US-US NUMBER OF SEQ ID NOS: 5 S SEQ ID NO 2 T.FRACTH: 6330		; NAME/KEY: unsure ; LOCATION: 5357, 5448 ; OTHER INFORMATION: nucleotide not determined US-09-880-427-2	Query Match 1.8%; Score 49; DB 3; Length 6330; Best Local Similarity 56.5%; Pred. No. 0.0013;

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390653 ATTTGTGTTTTATTAAATCTGTAATTTTTTCCCTGTCTATAAAAATATTTAGATTT 390594 1103 TGGAAATTTGTTTGCTCTTACGCCAACATAATATTTGATTTTGCCTCTTGGCTCTGAAAGC 1162 1142 1082 1163 CCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221 20 İGTAAACIGTIATAAGIACTIGATAATATATATITIGI KÜÜLÜGÜ 80 TTAAAATATTAACTCTCTCTCCCCTTTAAGAAAAAACGTGCTGAACCCCCTGCTCTAGATC 138 APPLICANT: Giordano, J.Y. APPLICANT: Giordano, J.Y. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG CURRENT APPLICATION NUMBER: US/09/513, 999C CURRENT APPLICATION NUMBER: US/09/513, 999C CURRENT APPLICATION NUMBER: US/09/513, 999C FRICK APPLICATION NUMBER: US/09/513, 999C SOFTWARE: Patent DATE: 2000-02-24 PRIOK FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: Patent Pm SOFTWARE: Patent Pm SOFTWARE: Patent Pm 1023 TTCTTATTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGA 1083 TTTTATCAATTTTAAAATTGTGGAAATTTGCTTTGCTCTTACGCCCAACATAATATTTGATTT Gaps 0; Gaps 1.5%; Score 42.6; DB 4; Length 640681; 59.5%; Pred. No. 3.7; cive 0; Mismatches 49; Indels 0; ö APPLICANT: SHIGENOBU, SHUJI APPLICANT: SHIGENOBU, SHUJI APPLICANT: WATANABE, HIDEMI APPLICANT: WATANABE, HIDEMI APPLICANT: SAKAKI, YOSHIYUKI TITLE OF INVENTION. GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS FILE REFERENCE: 081356/0159 Score 47; DB 4; Length 265; Pred. No. 0.0005; 45; Indels 0; Mismatches CURRENT APPLICATION NUMBER: US/09/790,988 CURRENT FILING DATE: 2001-02-23 PRIOR APPLICATION NUMBER: UP2000-107160 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PATCHIN Ver. 2.1 GENERAL INFORMATION: APPLICANT: Dumas Milne Edwards, J.B. Sequence 1, Application US/09790988 Patent No. 6632935 GENERAL INFORMATION: 1.78; ; OTHER INFORMATION: k=g or t US-09-513-999C-27278 Query Match 1.5 Best Local Similarity 59.5 Matches 72; Conservative 74; Conservative ORGANISM: Homo sapiens NAME/KEY: misc feature ; TYPE: DNA ; ORGANISM: Buchnera sp. US-09-790-988-1 Duclert, A. Query Match Best Local Similarity Matches 74; Conserv 1143 T 1143 640681 US-09-790-988-1/C ŝ 265 APPLICANT: LOCATION: TYPE: DNA SEQ ID NO 1 FEATURE : LENGTH: LENGTH: RESULT 8 S q  $\hat{o}$ g q qq  $\mathcal{S}$  $\mathcal{S}$ à A PPLICANT: GONG, Fangcheng et al. TITLE OF INVENTION: ISOLATED HUWAN DEHYDROGENASES, NUCLEIC TITLE OF INVENTION: ISOLATED HUWAN DEHYDROGENASES, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOOIO54DIV CURRENT APPLICATION NUMBER: US/10/118,037 CURRENT PELLOATION NUMBER: US/10/118,037 FRICE APPLICATION NUMBER: 09/740,028 FRICE APPLICATION NUMBER: 09/740,028 16677 TACAAGCTGATAATGGTTTTTTTTTTTTTAATGGTTACATTGTAAACTGTTATATAG 16736 16737 TACCTGATAATATCATTAATTTTGTTTGTTGCCTGCCATGCTTAAAATATTTAACTCTCT 16796 16736 16796 1120 1180 1180 ö ö 1061 TACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGGAAATTTGTTGGTCT 1120 1121 TACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCCAAAATATTTACCGTCT 16677 TACAAGCTGATAATGGTTTTTTTTTTTTTTAAATGGTTACATTGTAAACTGTTATATAG 1121 TACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCT Gaps Gaps :0 ö Query Match 1.8%; Score 49; DB 4; Length 19806; Best Local Similarity 56.5%; Pred. No. 0.0031; Matches 91; Conservative 0; Mismatches 70; Indels DB 4; Length 19806; Query Match 1.8%; Score 49; DB 4; Length 198 Best Local Similarity 56.5%; Pred. No. 0.0031; Matches 91; Conservative 0; Mismatches 70; Indels 16797 Geccertraggagagagagecercercerectederc 16837 16797 GGCCCTTTAAGAAAAAACGTGCTGACCCCTGCTCTAGATC 16837 1181 AGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221 1181 AGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221 0; Mismatches SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 OTHER INFORMATION: n = A, T, C or G Sequence 3, Application US/10118037 Patent No. 6797499 GENERAL INFORMATION: (19806) NAME/KEY: misc\_feature LOCATION: (1)...(19806 NUMBER OF SEO ID NOS: 4 , NAME/KEY: misc\_feature TYPE: DNA ORGANISM: Homo sapien кезинт 7 US=09-513-999C-27278 TYPE: DNA ORGANISM: Human 19806 LENGTH: 19806 RËSULT 6 US-10-118-037-3 LOCATION: LENGTH : FEATURE ð : A ÅÖ. ad ş ġ qq qa SN 0 ୁନ୍ଦୁ 8  $\delta$ 

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QY         1161         GCCCAAAATAT         1171           Db         203         GCCTAAACTTT         193	RESULT 11 US-09-513-999C-11322/c Sequence 11322, Application US/09513999C Fatent No. 6783961 GENERAL INFORMATION: APPLICANT: Duclert, A. APPLICANT: Duclert, A. FILE REPREMENT APPLICATION NUMBER: US/09/513,999C CURRENT APPLICATION NUMBER: US/09/513,999C FILE REPREMENT APPLICATION NUMBER: US/09/513,999C CURRENT APPLICATION NUMBER: US/09/513,999C	<pre>presentation provide the second provided by the second by the second provided by the s</pre>	Db       201       ACTGAGGAGCTCGGCCCAGCAGGGGGGGCGCGGGGGGGCGCAGTGGGGGCA       142         Qy       810       AGGGGAAGTTTTCAGGCCTTCATCAAGAGAAACAACTCTCCAGGCGGGGGCCAGTGGGGGCA       869         Db       141       GAGTAATTCAGGCCTTCATCAAGAGAAACCATCCTCAGGCTCGGCAGCGCCTCATC       869         0y       810       GAGGTAATTCCTCAGGGACACCGGGGGAAATCCATCTCCAATCTCCGGCCACTCCTC       820         0y       870       CTGTAATCGGGTGTGTGGGGGGGGCGCGGGGCAGGCAAGGCATGGGCAGGGACTTCCGGCGTTGCGGTGGGCTTGCGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG	RESULT 12 US-09-513-999C-23077 Sequence 23077, Application US/09513999C Sequence 23077, Application US/09513999C GENERAL INPORMATION: APPLICANT: Duclert, A. APPLICANT: Duclert, A. APPLICANT: Duclert, A. APPLICANT: Giordano, J'N. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961 FILE REFERENCE: 59.052.REG CURRENT APPLICATION NUMBER: US/09/513,999C	CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR PILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: Patent.Pm SEQ ID NO 23077 LENCTH: 398 TYPE: DNA CRCANISM: Homo sapiens FRATURE: misc_feature LOCATION: 144
Db 390593 T 390593	RESULT 9 US-09-248-795A-12137 Sequence 12137, Application US/09248796A Fatern No. 6747137 GENERAL INFORMATION: PATILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-13 CURRENT FILING DATE: 1999-02-13 FRIOR FILING DATE: 1998-02-13 PRIOR FILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US 60/074,725 FRIOR APPLICATION NUMBER: US 60/074,725 FRIOR FILING DATE: 1998-02-13 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1998-08-13 FRIOR FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1998-08-1	Query Match1.5%Score 41.6; DB 4; Length 210;Best Local Similarity67.0%; Pred. No. 0.018;100Matches59; Conservative0; Mismatches29; Indels0;Qy1011 CAAAAAAATTCTTATTTTTAGTAGCATGTATTTACCAAAAATGTACTCAATTA1070Qy1011 CAAAAAAAATATCTAATTTTTAGTAGCATGGTTTTAAGAAAAATGTACTCAAATTA1070Qy1011 CAAAAAAAAATAATCTAAATTTTTAACCAGGGTTTTAAGAAAAAAAA	ល លេក ហ	FILE RFERENCE: 59.US2.REG CURRENT FILING DATE: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: Patent.pm SEQ ID NO 10733 LENGTH: 329 TYPE: DNA ORGANISM: HOMO SADIENS US-09-513-999C-10733	Query Match1.5%Score 41.4;DB 4;Length 329;Best Local Similarity62.6%;Pred. No. 0.03;46;Indels3;Gaps1;Matches82;Conservative0;Mismatches46;Indels3;Gaps1;Oy1044TATTACCAAAAATAGTATTATGATTATGATTTATCAATTAAAAATGT110311

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GENERAL INFORMATION: APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ADE TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132 473396 TAAAAGTGTTCCTAAATTATGAAATAATTTTTAAAAATTAACATTTTAACAAATTAGAAA 473455° 1040 CATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAA 1099 1034 Page 0; Gaps Gaps Length 640681; .: 0 1.4%; Score 39.6; DB 4; Length 1107; llarity 52.4%; Pred. No. 0.26; Conservative 0; Mismatches 79; Indels 0 APPLICANT: HATTORI, MASAHIRA APPLICANT: SAKAKI, YOSHIYUKI TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS Score 40.4; DB 4; Length 6 Pred. No. 17; 0; Mismatches 71; Indels 473456 rcagraarrarcrirtrorrcriftaaaraa 473489 1100 TTGTGGAAATTTGTTTGCTCTTACGCCAACATAA 1133 CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 FRIOR APPLICATION NUMBER: US 60/074,725 PRIOR FILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR APPLICATION NUMBER: US 60/096,409 NUMBER OF SEQ ID NOS: 28208 FILE REFERENCE: 081356/0159 CURRENT APPLICATION NUMBER: US/09/790,988 CURRENT FILING DATE: 2001-02-23 CURRENT FILING DATE: 2001-02-23 PRIOR APPLICATION NUMBER: JP2000-107160 PRIOR FILING DATE: 2000-04-07 US-09-248-796A-8906/c ; Sequence 8906, Application US/09248796A ; Patent No. 6747137 Sequence I, Application US/09790988 Patent No. 6532333 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: SHIGENOBU, SHUJI Query Match 1.5%; Best Local Similarity 53.9%; Matches 83; Conservative C HIDEMI SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 Candida albicans ::: ::::| 413 WYWKMDMDWBG 423 ; TYPE: DNA ; ORGANISM: Buchnera sp. US-09-790-988-1 WATANABE, NUMBER OF SEQ ID NOS: Best Local Similarity Matches 87; Conserv US-09-248-796A-8906 LENGTH: 640681 1107 RESULT 14 US-09-790-988-1 SEQ ID NO 8906 APPLICANT: TYPE: DNA ORGANISM: Query Match LENGTH: RESULT 15 g å S g PD DD 8 8  $\delta$ q ; 0 1131 TAATATTGATTTTGCCTCTTGGCTCTGAAGCCCCAAAATATTTTACCGTCTGCCCGTTAC 1190 ö 1205 GACTACTGAGCCAGACCTCCATTACCTCCATCCTGTTGGATTATTATAAGAAAGCCTCA 1264 1265 GACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGGCAGGGGAA 1324 1025 CTTATTTTTGGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGATT 1084 1085 TTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGATTTTG 1144 1145 CCTCTTGGCTCTGAAAGCCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAGTCTGCT 1204 197 TAGTTATGACAGAACCTCTATGGCCACAAAGTTTAAAATATTTACTATCTTGCTATTTAC 256 53 MSKSRKWTWARMYCKYRRWYNKSRWWKGWYKKWYBCANNTSBRYHARMKUCKYRRWYNNKSRWWYKGWYKKWYBCANNTSBRYHARWKTAYBM 112 113 TMTNKWGKTGWRHRYWRWRAMBDTVDHHYVTAMNNAWTTMCMMDKDDKRTRWWKKONNA 172 293 KYWGWNRABVNSTCTTWKSKTTKVRTSCWANNCRAGDANKDHKWWKWSAAMGVYWNNNN 352 Gaps 0; Gaps APPLICANT: The University of British Columbia TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants FILE REFERENCE: 4810-58741 CURRENT APPLICATION NUMBER: US/09/806,708B CURRENT APPLICATION NUMBER: US/09/806,708B CURRENT FILING DATE: 2001-04-03 FRIOR APPLICATION NUMBER: US 60/147,133 REIOR APPLICATION NUMBER: US 60/147,133 REIOR APPLICATION NOMBER: US 60/147,133 REIOR APPLICATION NUMBER: US 60/147,133 REIOR SEQ IN NOS: 23 REIOR SEQ IN NOS: 23 SOFTWARE: PatentIn version 3.0 :0 Query Match 1.5%; Score 40.4; DB 4; Length 1141; ,Best Local Similarity 9.4%; Pred. No. 0.15; ,Matches 35; Conservative 167; Mismatches 169; Indels 0 Score 40.8; DB 4; Length 398; Pred. No. 0.052; 0; Mismatches 37; Indels 0 1191 AGAAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACC 1230 257 AGAAAATATTTGCTGACTTCTGCCCTACAGAAACATAAGC 296 Sequence 22, Application US/09806708B Patent No. 6784342 بد OTHER INFORMATION: n=a, g, c or ch 1.5%; 1 Similarity 63.0%; 63; Conservative ( TYPE: DNA ORGANISM: Artificial sequence UCS-07HER INFORMATION: m=a or c Query Match Best Local Similarity Matches 63; Conserv W Sequence 22, Applicat F Fatent No. 6784342 GENERAL INFORMATION: RESULT 13 US-09-806-708B-22 LENGTH: 1141 V SEQ ID NO 22 8 <u>a</u>\_\_\_\_ δŷ. đ 199 đ ମ୍ ଜୁନ୍ଦୁ ଅନ୍ ð d d ð ::: qq q  $\delta$ ð  $\delta o$ 6 q ð

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2119 GAAGTCAACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2179       GGTTGAGCTTCCTGGTGCGGGTCCCGGTCCCACTTGCAGTTGGTCTCTGGTTAGG       2238         2111       2111       1111<	Green control of the	1	2479       AGATTGGGTGACTCTTTTCTAAAGGTGGGGGGGGGGGGG	202 GATEGGGTENGGTENGTENTIAL AND	2659 CGGACGAGAAGTCTGTATGTGGGATCTGTGGGTTGGGGTTAGAATGCAAATAAACTCACAT 2718 %	2719 TTGTAAGAAAAAAAAAA 2739                   22 TTGTAAGAAAAAAAAAAA 2	BU684754 685 bp mRNA linear EST 07-OCT-2002 UT-CF-ENL-acv-d-09-0-UL 31 UT-CF-ENL Homo sapiens cDNA clone BU684754.1 GI:23538028 BU684754.1 GI:23538028 BU684754.1 GI:23538028 BG684754.1 GI:23538028 BG684754.1 GI:23538028 BG684754.1 GI:23538028 BG684754.1 GI:23538028 BG684754.1 GI:23538028 BG684754.1 GI:23538028 BG684754.1 GI:23538028 BG784754.1 GI:23558 BG784754.1 GI:2558 BG784754.1 GI:25588 BG784754.1 GI:25588	1 (bases 1 to 685) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery Gencne Res. 6 (9), 791-806 (1996) 9904477	8889548 Contact: McCray, PB McCray Lab University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA 2024 University of Iowa 701: 319 356 4866 Fax: 319 356 7171 Email: paul-mccray@ujowa.edu Tissue Procurement: Dr. M. J. Welsh, University of Iowa
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	3 7/c CB242367 TON UI-CF-FN0-age-m-22-0-UI.s1 UI-CF-FN0 Homo sapiens CDNA Clone UI-CF-FN0-age-m-22-0-UI 3', mRNA sequence. ON CB242367.1 GI:28364011			MCTay Lab University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA 721: 319 356 4765 Fax: 319 356 7171 Email: paul-mccray@uiowa.edu	CDNA Library preparation: Dr. W. WENTO, DI LUWA CDNA Library preparation: Dr. W. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems		source 1766 /organism="Homo sapiens" /mol_type="mRNA" /db_treft"taxon:9606	<pre>/tissue type="two-age="curve.rule" /tissue type="twman tung Epithelial cells" /lab_host="DH10B (Life Technologies) (T1 phage resistant)" /clone lib="url-cp-pro" /note="drgan: Lung; Vector: pT713-pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; Url-Cr-Pro" is a subtracted CDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, hennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-scares@ulowa.edu TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS fAr to LPS 24M</pre>	TAG_IEB=CI-CF-FN0 TAG_SEQ=CTGCTCAGGT" tch 24.7%; Score 680.4; DB 6; Length 766; al Similarity 97.6%; Pred. No. 9.6e-168;	723; Conservative ( 999 GTAACAGTAGTGATAGCAGG 999 GTAACAGTAGTGATAGCAGG 736 GTAACAGTAGTGATAGCAGG 059 CAGCTTCTCACTCGATCCT 611 CAGCTTCTCACTCGATCCT 611 CAGCTTCTCACTCGATCCT
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Db265TCATGCCTTCGTCCTGAGGAGCCCTGAGGTGGGGGGGGGG	RESULT 5 BQ953674 BQ953674 DCCUS DEFINITION DEFINITION ACROCUT 8003100 Lupski_sciatic_nerve Homo sapiens CDNA clone NAGES:6196871 5', mRNA sequence. ACCESSION BQ935674.1 G1:22369152 ACCESSION BQ935674.1 G1:22369152 KEYWORD HOMO sapiens (human) ORGANISM HOMO SAPIENS HOMO SA	<pre>cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13611 row: d column: 08 High quality sequence stop: 600. FEATURES 1.642 Location/Qualities fource //doalities /db Zref="texaon:9606" /db Zref="texaon:9606" /doave="scitation" / db Zref="scitation" /doave="scitation" / doave="scitation" /doave="scitation" / doave="scitation" /doave="scitation" / doave="scitation" / doave="scitation</pre>	<pre>//iab_host="PHIOB" /</pre>
<pre>CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resegen.com) or from Open Biosystems (www.openbiosystems.com). Seq primer: M13 PORWARD New openbiosystems: com). Seq primer: M13 PORWARD POLYAFIES 1. G85 1. G85 1. G85 1. G85 1. Creation/Qualifiers 1. G85 1. G85 1. Creation/Qualifiers 1. Creation/Qualifiers 20LYAFIES 1. G85 1. Creation/Qualifiers 20LYAFIES 20LYAF</pre>	<pre>/dimensional contains and contained on the contained on the contained polylinker; site 1: BCoR I; Site 2: Not I; /note="Cream: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; site 1: BCoR I; Site 2: Not I; UT-CF-ENN is a normalized cDNA library containing the following tissue(s): primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Scares (Genome Research, 6: 791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligted to an ECoR I adaptor; digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand DNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is cTGCTCAGGT. TAG IISSUB-Hunn Lung Epithelial Cell Lines untreated LPS 6hr To LPS 24h TAG IISSUB-Hun Lung Epithelial Cell Lines untreated LPS 6hr To LPS 24h</pre>	Query Match23.8%; Score 655; DB 5; Length 685;Best Local Similarity98.5%; Pred. No. 4.7e-161;Matches 669; Conservative0; Mismatches 9; Indels 1; Gaps 1;Qy345 AgGGACAGGGCTTGAGGGCCAGTGAGGGCCTGGGGCCCCAGGGCCCCCAGGGCCCCTGGGGCCQy345 AGGACAGGGCTTGAGGGCCAGTGAGGGCCGGGGGCGCGGGGCGCCGGGGCCCCCAGGGCCCCCAGGGCCCCCAGGCCCCCC	QY525GCAACTGGTGTGTGTGGTGGGGGGGGGGGGGGGGGGGGG

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2589 AAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTTGCACTTGTTACTG 2648 	2649 TAC 2651		Н Н Н Н Н Н Н Н Н Н Н Н Н Н Н Н Н Н Н	Homo sapiens vience. Homo sapiens vience. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 640) Ronaldo, M F. Lennor, and Soares.M.B.	Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996)	97044477 8889548 Contact: McCray, PB	McCray Lab University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA 7e1: 319 356 4866 Fax: 319 356 4171 Emmil: paul-mccray@uiowa.edu Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).	- LOL	Cells" (dev Etage="Adult" /lab_host="DH10B (Life Technologies) (T1 phage resistant)" /clone_lib="UI-CP-EN1" /clone_lib="UI-CP-EN1" /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinkrer; Site 1: EcoR 1; Site 2: Not 1; UI-CP-EN1 is a normalized_CDNA library containing the following tissue(s): Primary Lung Cyetic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soars, Genome Research, 6;791-806,	1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand CDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT. TAG TISUES Human Lung Epithelial Cell Lines untreated LPS first_to LPS 24h TAG_LDB-UI-CF-ENI TAG_LB-UI-CF-ENI
QY 25 Db	QY 26	27	RESULT 7 BQ045123/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SCUTCE	2 13 1	TITLE JOURNAL	MEDLINE PUBMED COMMENT		FEATURES source		

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943 GTTTATGCCACTGATTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTC 1002 EST 26-JUN-2003 ö ibirary in the pCWVSPORT6 vector(Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript essentially following the protocols of the SuperScript flasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGAGGGGCGCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)." 265 CTCATGCCCTTCGTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGGCCAGGGGAGGTTTTCA 206 883 205 GGCCTTCATCAAAGAAACAACATCCTCAGCTCCGCACCCCCTCATCCTGCACTT 146 884 ACC-GGTGTGTGTGCCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCT 942 ترمينية (11 bp mRNA linear BST 26-JUN-200: 2018908/91 Human lacrimal gland, unamplified: oj Homo sapiens cDNA clone oj28908 5', mRNA sequence. /tissue type="lacrimal gland" /dev stage="Adult" /lab\_host="EMDH10B" /loce=lib="Human Earimal gland, unamplified: oj" /note=lib="Hye; Vector: pCMV5port6; RNA was extracted from 2 human lacrimal glands. A directionally cloned cDNA 145 ACCNGGTGTGTGACGCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCT 86 85 GTTTATGCCACTGATTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTC 26 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 824 GGCCTTCATCAAGGGGAACAACATCCTCAGGTCCGCACCCCTCATCCTGTATCAGGACTT Gaps Dickinson, D., Laurie, G. and Wistow, G. Expressed sequence tag analysis of human lacrimal gland Unpublished (2002) ö Query Match 21.9%; Score 604.2; DB 6; Length 611; Best Local Similarity 99.5%; Pred. No. 1.1e-147; Matches 606; Conservative 0; Mismatches 3; Indels 0. Section on Molecular Structure and Function National Eye Institute 6/31, NH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 28 row: 9 column: 08 Seq primer: M13RP1 reverse primer (ABI) /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="oj28g08" Location/Qualifiers CCCCATCACAAAAAAAA 1022 φ CD723979.1 GI:32274833 25 CCCCATCACAAAAAAAAA sapiens (human) (bases 1 to 611 Contact: Wistow G 1. .611 Homo sapiens Homo EST 1003 source DEFINITION **ORGANI SM** AUTHORS TITLE JOURNAL COMMENT ACCESSION RESULT 9 CD723979 VERSION KEYWORDS SOURCE REFERENCE FEATURES ORIGIN LOCUS ß g g ą qq 8 5  $\mathcal{S}$ 8 /dev stage="Adult"
/lab\_nost="DH10B (Life Technologies) (T1 phage resistant)"
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modified polylinker; Site\_1: EcoR I; Site\_2: Not I;
UT-CF-ENN1 is a normalized CDNA library containing the
following tissue(S): Primary Lung Cystic Fibrosia the
following tissue(S): Primary Lung Cystic Fibrosia the
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1996. First strand CDNA synthesis was primed with an
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cDNA was ligated to an EcoR I adaptor; digested with Not
I, and cloned directionally into pT773-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand CDNA contains a library tag sequence that is
located between the Not I site and the (d7)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG TISCUE-Human Lung Epithelial Cell Lines untreated LPS
choored to an extend Coll. 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Fax: 319 356 4866 Fax: 319 356 7171 Email: paul-mccray@uiowa.edu Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Prreparation: Dr. M. Bento Soares, University of Iowa CDNA Library Prreparation: Dr. M. Bento Soares, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CONA Library Preparation: Dr. M. Bento Soares, University of Iowa Cone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems i, 463 566 464 AAAGCTCCTCCTGGCTTTCCTCCCCCCAATCTATGGGTCACAGGCTAACAGATCTGAG 523 583 505 GGCAACTGCTGCTAGTGGCCCGGGGCTGCCCTGCCCGGGCTCTGCCGCCTCTTAGG 446 703 565 AAAGCTCCTCCTCGCTTTTCCTCCCCCCCAATCTATGGGTCACAGCTAACAGATCTGGG 506 GCCTTCTAGAGGCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTG 643 GCCTTCTAGAGGCAGTGTCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTG 386 763 CAGGCCAGCTGATGGGATAAGGTGGGGAAGGACGGTCAGTGGTGGCCAGCTGGCCAGCTGGCCA 326 325 GCCTGGCGATGGGGAAACCAAACCATGTCCCCCCAGCGAAGGGCCAGGTGGGAACCTGTC 266 764 CTCATGCCCTTCGTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGGCCAGGGGAAGTTTTCA 823 CTGCCCAGGGGCACCCTGAGGCTCCTGAAACCCCCCACTTAGCTTCCAGACCTTTCTGCA CIGCCCAGGGGCACCCTGAGAGCTCCCGGAAACCCCCCACTTAGCTTCCAGACCTTTCTGCA GGCAACTGCTGTGCTAGGCCAGGGCTGCACCTGCCATCCCCGGGCTCTGCCACTTTAGG CAGGGCAGCTGATGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCA /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="UI-CF-EN1-aed-n-21-0-UI" /clssue\_type="Primary Lung Cystic Fibrosis Epithelial GCCTGGCGATGGGGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTC 1; Gaps Length 625; 0; Indels Score 608; DB 6; L Pred. No. 1.1e-148; 0; Mismatches .. .625 'organism="Homo sapiens" Location/Qualifiers IAG\_SEQ=CTGCTCAGGT" LIB=UI-CF-EN1 (www.openbiosystems.com) Seg primer: M13 FORWARD POLYA=Yes. to LPS 24h 22.1%; 99.8%; Matches 619; Conservative Cells" Similarity Query Match Best Local S 404 625 524 584 445 644 385 704 source REATURES ORIGIN ĝ, 8 q qq. dū'' ð ð g ð. 8 qq 8 ð

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<pre>167 GCACTGGGCGATGTCCCCAGAGGCAGGGCAGGTCTCTAGAGGGGGGGTCTCCCCACATGACTG 226 1                                   </pre>	227 GCTTCACAGGGCACTTCGGGGTTGGGGTTGCTGTGTGTGT	287 TGCAGGTAGGAAATGTTTGTACCCTCTTCTGATTGCCACCCCCTTCGCCCCTTAG 346 	347 GGACAGGGCTTGAGGGCCAGTGAGGGGCTGGTCAGGCACCCCAGGCCTCCTTGGGGACCTG 406 	407         CCCAGGGGCACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACTTTCTGCAAAA         466           111111111111111111111111111111111111	<pre>467 GCTCCTCGGGCTTTCCTCCCCCCAATCTATGGGCTCACGGCTAACAGATCTGAGGGC 526 1                                    </pre>	527 AACTGCTGTGCTAGTGGCCAGGGCTGCCACCTGCCACCCCGGCTCTGCCACTTTAGGGCC 586 	587 TICTAGAGGCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGCTTTCTGCTCCTGTGCAG 646 	647         GGCAGCTGATGAGGAAAGGACGGCAAGGACGGCTGGGCCGGCC	707         TGGCGATGGGGGAAACCATGTCCCCCAGGGAAGGGCCAGAGTGGGAAACCTGTCTC         766           111111111111111111111111111111111111	67 A	<pre>C A1928242 MN W055h01.X1 NCI mRNA sequence. A1928242 GI A1928242 GI BST. A1928242 GI BST. BST. HOMO BADJENS ( HOMO BADJEN</pre>
ζ ζ	QY Db	vy da	νο dα	λο q	yo du	δ Δ	QY Db	AD da	AQ AQ	ov T	RESULT 10 A1928242/c DEFINITION ACCESSION VERSION VERSION KEYWORDS OURCE OURCE AUTHORS TITLE TITLE COMMENT

2209 2269 2389 2449 2508 2568 2628 2629 ATATTTTGCACTTGTTACTGTACCATAGTGCGGGACGAGAAGTCTGTATGTGGGATCTGTG 2688 BM019092 768 bp mRNA linear BST 30-OCT-2001 603647129F1 NIH\_MGC\_98 Homo sapiens CDNA clone IMAGE:5428711 5', mRNA sequence. BM019092 2329 Ä 518 398 338 278 218 217 GEAGTATCTCTCTCGGGCTGTGGTCGCCCTTGGATGGGTCGGGTGTGAGGTCCTGG 158 458 98 8 8 157 GGAGGGGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGC 97 ATATTTTGCACTTGTTACTGTACCATAGTGCGGGACGGAGGAAGTCTGTATGTGGGGATCTGTG GOTOCCACAGOTACTGATGGCCCGGGCCAGGTTGAGCTTCCTGGTGTCCCGGATCC 457 CTGTCCTGAGGCCTCATTGCTGGGCTGGGGTGTGCTGGGGAAAAGCTTTGCGGGGCTT 337 CCTGGGTGGGAGGCTACTGCTGTGTTCTCTATGTTCTGTGTTTTAAATGATTTCTTT 2569 GGAGGTGGGCGTTGAGCTCCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGC 577 GGTCCCACAGCTAGCTGATGGCCCGGAGCTAGGTTGCAGGTTCCTGGTGTCCGGATCC 2210 CACTTGCAGATCTCATGCTCCAGATAGGTGGGGGACAAGTTCTTTTGTCACAGTGCTGGCT 2330 GCTTGGTTAACCACAGAAGAAGAGAGGGGACTGTTTGGGGGTGCCTCTCTGCAGCCTCCCCGT 2390 GCTGGGTGGAAGCACGGTTACTGTGTTCTCTCTTAAAAATGTTTCATGATTTCCTTT CTAAAGATGTAACCTCCACACCTTTCTCCCAGATTGGGTGACTCTTTTCTAAA-GGTGGTG 517 CACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGATCTTTTTGTCACAGTGCTGGCT 1; Gaps Query Match20.5%;Score 563.4;DB 1;Length 577;Best Local Similarity99.7%;Pred. No. 6.5e-137;Matches 575;Conservative1;Matches575;Conservative0;Mismatches1;Indels1; 2450 2150 source DEFINITION RESULT 11 BM019092 ACCESSION FEATURES ORIGIN LOCUS g q  $\delta$ q q  $\delta$ g  $\mathcal{S}$ q  $\delta d$ å  $\mathcal{S}$ g  $\delta$ q g 8  $\delta$ 8 8

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	TTGGCTTCTCGGGG TTGGCTTCTCGGGGG 	AGGGGACTGCTCAC-               AGGGGACTGATCACA	CCTCCATAAGGGTAT                CCTCCATAAGGGTAT	o mRNA linear P-DUL Homo sapiens	י סלדני א מלדני	Craniata; Vertebrata; Eutel Catarrhini; Hominidae; Homo	tres,M.B. two approaches	l6)	s, Iowa City, IA	elsh, Universit	M. BENCO SOAFES I. BENTO SOAFES, O SOAFES, Unive S may obtain cl	Genetics (www.resgen.com) or irom Upen Blogystems (www.openbicsystems.com). (me following repetitive elements were found in this CDNA sequence: 188-250, _>MERSBB#DNA/MER1_type (matched compliment)			rechnologies)	tte_1: EcoR 1/ 1 zed_cDNA library rimary Lung Epil	d according to 1 h, 6:791-806, 1 med with an olig e. Double strai	digested with No T3-Pac vector, 7
	GGGGACTGAGGACCT GGGGACTGAGGACCT GGGGACTGAGGACCT	getettectgetaca                getettectgetaca	cceccccccce          BAGCCGACACACCGG	8926 577 bp mRNA F-DU1-abc-n-17-0-UI.S1 UI-CF-DU1 Homo	GI:23526358 s (human)	zoa; Chordata; ( ria; Primates; (	577) ennon,G. and Soa nd subtraction:		, FB Dwa Of Iowa Med Labs,	sb 71 ray@uiowa.edu ent: Dr. M. J. V	reparation: Jr. rrayed by: Dr. b by: Dr. M. Bent cion: Researcher	ssgen.com/ or ri cems.com). repetitive eleme 50, >MER58B#DNA/	r: M13 FORWARD Location/Qualifiers 1. 577	organısm="Homo sapiens" mol_type="mRNA" db_xref="taxon:9606" clone="UI-CF-DU1-abc-n-	<pre>cype="trimary cage="Adult" sst="DH10B (Life lib="UI-CF-DU1"</pre>	Organ: hung; ve ed polylinker; s JUT is a normali ing tissue(s): E	/ was constructe / Genome Researc /nthesis was pri /ing a Not I sit	ScoR I adaptor, ionally into pT7
			1 TGGTTTTTGAGGGG       2 AAGGAAAAGAGAG	BU678926 UI-CF-DU1-abc-n	BU678926 BU678926 BU71 BU71 BU71 Homo sapiens (human)	Homo sapiens Eukaryota; Meta Mammalia; Euther	<ol> <li>(bases 1 to 577)</li> <li>Bonaldo,M.F., Lennon,G. and Soares,M.B.</li> <li>Normalization and subtraction: two approdiscovery</li> </ol>	Genome Res. 6 (9 97044477 8889548	Contact: mccray, PB McCray Lab University of Iowa 2024 University of I	Tet: 319 356 71 Fax: 319 356 71 Email: paul-mcci Tissue Procureme	CDNA LIDEALY DI CDNA LIDEALY A DNA Sequencing Clone Distribut	Genetics (www.re (www.openbiosyst The following 1 sequence: 188-29	seq primer: ML3 FORWARD POLYA=Yes. Location/Quali 1577	/mol_ty /db_xre /clone=	/ dev_su / dev_su / clop_ho	/noce modifié UI-CF-I followi	LIDTAT) Soares, CDNA sy CONTAIT	to an E directi
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Ganome Sequencing Center DIAD Sequencing by: Washington University Genome Sequencing Center CDIAD Editribution: NGT-CGAP Clone distribution information can be found through the I.M.A.G. E. Consortium/LML at: New-bio.llnl.gov/bbpy/image/image.html Seq primer: -400P from Gibco High quality Sequence Stop: 443 Location/Qualifiers Source 1. 547 Arganism="Homo sapiens" (AD_Ltype="mRNA" AD_Ltype="mRNA" (AD_Ltype="mRNA"	Outery Match19.8%; Score 546; DB 2; Length 547; Best Local Similarity Best Local Similarity 99.8%; Pred. No. 2.5e-132; Matches 546; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Cy 2179 GGTTGAGCTTCTGGGTGCCAGTCGGATCCATTGCGGATCTCAGCTCTCAGTTCGGTCTCAGTCGGATCCAGATCAGGCTCACTCA	Qy2479AGATTGGGTGACTCTTTTCTAAGGTGGGGGGGGGGGGGG
used to prime the synthesis of first-strand CDNA contains a library tag sequence that is located between the Not I site and the (d7)18 tail. The sequence tag for this library is GGGTG7AGGC. Tag TISSUB-Lung Epithelial Cells Tissue nos 359-368 Tag_LIB=UL-CF-DU1 Tag_LIB=UL-CF-DU1 Tag_EpiSeGGGCTGAGGC Match SEG_SEGGGCTGAGGC Match Sectoral Similarity 99:58; Pred. No. 4.6e-136; Matches 562; Conservative 0; Mismatches 3; Indels 0; Gaps 0; 9 11 TragTAGACCAATGAAATATGTACCCAATAAAAAAAAAAAAAA	Qy1211TgaGGCGAGACCTCATTACCTCCATTACTTGATGATTATTTAAGAAAGCCTCAGACAGT1270Db249TGAGCCAGACCTCCATTACCTCCATCCTGTTGGATTATTTTAAGAAAGCCTCAGACAGT308Qy1271AAGGGCTTTTTTAAAGCATTACTTGCTTGGGTTGGAAGCAGGGGAAGCATTC308Qy1271AAGGGCTTTTTTAAAGCATTAGCTTGGTTTGGCTTGGAAGCAGGGGAAGCATTC308Qy1331AGATGAGCTTTTTAAAGCATTAGCTTGGCTTTGGCTTGGAAGCAGGGGAAGCATTC368Qy1331AGATGAGCGTTTTTTAAAAGCATTAACCCTGGCTTGGCT	<pre>RESULT 13 AW271767 = 547 bp mRNA linear EST 03-JAN-2000 DEFINITION = AW271767 = 547 bp mRNA linear EST 03-JAN-2000 DEFINITION = AW271767 = AW271777  = AW271777   = AW27177777 = AW271777777 = AW27177777 = AW27177777 = AW27177777 = AW27177777 = AW2717777 = AW27177777777777777 = AW27177777777777777777777777777777777777</pre>

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RESULT 14 RESULT 14 AMM73671/c AW173671 535 bp mRNA linear EST 16-NOV-1999 DEFINITION xj10908.x1 NCI CGAP_Ut2 Homo sapiens cDNA clone INMGE:2656862 3', REFINITION AM173671 AW173671.1 G1:6439619	<pre>MBDS EST BENDS EST BENDS BENDS (human) BENDS HEARS (human) BENDS PARTATORIA (TATAIATA) VETTEBRATATA, Butteleostomi, NUTSM FORM Satura (TATAIATA) VETTEBRATATA, Butteleostomi, BENDS 10 Dasses 1 to 535) HORS NCTCGAP http://www.ncbi.nlm.nih.gov/ncicgap. HORS NCTCGAP http://www.ncbi.nlm.nih.gov/ncicgap. HORS NCTCGAP http://www.ncbi.nlm.nih.gov/ncicgap. HORS NCTCGAP http://www.ncbi.nlm.nih.gov/ncicgap. The former and a material formation of the formation and the formation and the formation and the formation information can be numbrished (1997) NT Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. MT Statis (agabs-remain].nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CONM Library Preparation: Life Technologies, Inc. CONM Library Arreyed by: Grego Lannon, Ph.D. CONM Library Arreyed by: Grego Lannon, Ph.D. Cond through the I.M.A.G.E. Consortium/LLNL at: Namert 400T http://mage/image.html Source found through the I.M.A.G.E. Consortium/LLNL at: Migh quality sequence stop: 420. High quality Sequence stop: 42</pre>	Query Match       19.3%; Score 532.4; DB 2; Length 535;         Best Local Similarity       99.6%; Pred. No. 9.6%-129;         Matches       533; Conservative       0; Mismatches       2; Indels       0; Gaps       0;         2191       TGGTGTCCAGTCCGGATCCACATGCAGATCATCCTCTCGGATAGGTGGGACAAGTTC       250         2191       TGGTGTCCAGTCCGGATCCACATGCAGATCATCCTCTCGGATAGGTGGGACAAGTTC       250         535       TGGTGTCCAGTCCGGATCCACATGCAGATCAGGTAGGTGGGACAAGTTC       276         535       TGTTGTCCAGATCCAGATCCACATGCAGATCAGGTAGGTGGAGGACAAGTTC       276         535       TGTTGTCCAGGTCGGCATCTCACATGCTCAGGATAGGTGGGGAGCAAGTTC       276         2251       TTTTGTCAGGTGCTGGCTGGCTCGAGAGGGGCCTCATGGAGGGGGACGAGTCTCTCGCGG       216         2351       TTTTGTCACGGGCGGGGGGGGGGCCTCATGCGCGGGGGACGGGGGACGGGGGGGG

-1990 Scares, Ph.D. 2n, Ph.D. rsity Genome Sequencing Center distribution information can be ium/LLML at: teor: pT7T3D-Pac (Pharmacia) with tell: Not I; Site 2: Eco RI; malized library NCI CGAP KAI3 was were made in vitro. Following HAP is used as tracer in a subtractive the driver was PCR-amplified cDNAs is used From the same library i. 145607-1456775, and tion by Bento Soares and M. CTCAAGTTGTCCTACTGCCATGTTT 2610 ACTGTACCATAGTGCGGGACGAGAAGT 2670 RNA linear EST 29-NOV-1999 ans cDNA clone IMAGE:2695873 3', і. Г TGGTGTGCCCTTGGATGGGTCAGGT 176 SCTAACAGATCTGAGGGCAACTGCTG 534 GCTAACAGATCTGAGGGCAACTGCTG 479 CTCTGCCACTTTAGGGCCTTCTAGAG 594 ACTGTACCATAGTGCGGACGAGAAGT 56 tta; Vertebrata; Euteleostomi; hini; Hominidae; Homo. aluk, M.D., Ph.D., Michael R. /ncicgap. nome Anatomy Project (CGAP), AATAAACTCACATTTGTAAG 2725 ||||||||||||||||||| AATAAAACTCACATTTGTAAG 1 1; Gaps 2; Length 538; -127; 0; Indels

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0y       2341       CACAGAAGAAGGGGACTGTTTGGGGTGGCTCTTGCAGGCTCCCGGTGGGTG	RESULT 3 US-09-989-920-91/c Sequence 91, Application US/09989920 Facent No. US2002012957A1 GENERAL INFORMATION: APPLICANT: Recipon, Herve APPLICANT: Recipon, Herve APPLICANT: Recipon, Herve APPLICANT: Sci-Yu APPLICANT: Sun, Yonghua TTILE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and TTILE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and TTILE OF INVENTION NUMBER: US/09/989,920 TTILE OF INVENTION NUMBER: US/09/989,920 TTILE DFPLICANTE: 2001-11-21 CURRENT FILING DATE: 2001-11-21 CURRENT FILING DATE: 2001-11-21 STOFTWARE: PatentIn Version 3.1 SCOFTWARE: PatentIn Version 3.1 SEQ ID NO 91 CLANNIN: Homo sapien US-09-989-920-91	Query Match87.1%; Score 2397.4; DB 9; Length 2399; Best Local Similarity 100.0%; Pred. No. 0; Matches 2398; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy356 Tradaggecraferangecerageragecragecragecragecragecrageceragedaec tagge 11	Qy     416     ACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCGGAAAGCTCCTCCT     475       Db     2339     ACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCGGACCTTTCTGCAAAGGCTCCTCCT     2280       Qy     476     GGCTTTCCTCCCCCCCAATCTAGGGTCACAGGCTCTGGGGGGCAACTGCTGT     535       Db     2379     GGCTTTCCTCCCCCCCAATCTAGGGTCACGGCTAACGGGTCAGGGGGCAACTGCTGT     5220	536 GCTAGTGGCCAGGGCTGCCACCCCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGG 595 1
1201       TGCTGACTACTGAGCCAGACCTCATTACTACTCCTCCTGTTGGATTATTTAAGAAGGC       1261         1261       CTCGGAGCAGTAGGCCCTTTAAAGAATTAAATGACTTGGTTTGGGCTGGGCGGC	1681       Treacrretrogaccrrecadecorreroconterreconterreconcertacta       1740         1681       Treacrretrogaccrrecadecorrectorreconterreconterreconcertacta       1740         1741       Integerretrocadecorrecadecorreconterreconterreconcertacta       1740         1741       accostanterreconterreconterreconterreconterreconcertacta       1740         1741       accostanterrecontererreconterreconterrecon	2041       GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCTCCCTAAAGCAATGGGGAGGCCCC       2100         2041       GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTTAAAGCAATGGGGAGGCCCCC       2100         2041       GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCTCTAAAGCAATGGGGAGGCCCCCC       2100         2041       GTGTTCTGCGCATTTGGTCAGCTTCACGATCTCGATCCCCTTAAAGCAATGGGGAGGCCCCCC       2100         2101       CACTAGCCCAGTTTTCAGGAAGTTCACTGGAGGGTTAGATGGGGGGGCCAGGGGTCCCACAGC       2160         2101       CACTAGCCCAGTTTTCAGGAAGTTCACTGGAGGGTTAGATGGGGGGCCAGGGGTCCCCACAGC       2160         2101       CACTAGCCCAGTTTTCAGGAAGTTCAACTGGAGGGTTAGATGGGGGGCCAGGGGTCCCACAGC       2160         2101       CACTAGCCCCAGTTTTCAGGAAGTTCAACTGGAGGGTTAGATGGGGGGCCAGGGGTCCCCACAGC       2160	2161 TACTGATGGCCGGGGCGGGGTTGGGGTTGCTGGGTGCCGGGTCCCGGGTCCCGGGT 2220 1	281 CCTCATTGCTGGCTGGGTGGGTGGGTGGCTGGCTGGCTGG
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1676 1079 1736 1736	ACCTTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGC 1735 	
959 1856 899	CCTCCATAAGGGTATCCTGGGCCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACGGCC 900 CCTCCATAAGGGTACCCTGGGCCCTGAGAATTCTGCATCTGCCATTGGCAGGCA	
1916 839 1976 779	CTGTGGCCTTGTCCAGCCTGGTGCTCTTCACTCCAGGGGCAGCAGCAGC 1975 	
h m	TTGTGTTTTGGGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGGG 20	
2096 659	IAAGTCAJ	
2156 599	ACAGCTACTGATGGCCGGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCCAGTTG 2215	
2216 539	GTTCTTTTGTC             GTTCTTTTGTC	
2276 479	IGGGAAAAGCTTTGCGGGGGCTTGCTTGG 23.                                IGGGAAAAGCTTTGCGGGGCTTGCTTGG 42.	
2336 419	TTAACCACAGAAGAGAGAGAGAGAGATGGTTGGGGGGCGCCTCGCGGGGGGGG	
2396 359	AATGTTCATGTAT7               AATGTTCATGTAT7	
2456 299	AGATTGGGTGACTCTTTTCTAAAGGTGGTGGGGGGGGATAT 25                                     	
2516 239	GGATGGGTCAGGTGGGTGTC 	
2576 179	GCCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTGTACCTGAAATAAAGCATATTTT 2635 	
2636	GCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTAGGATCTGTGCGTTGGGT 2695	

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GTCCTQAGGAGCCCTGAGGTGGGCAGGGGGCCAGGGGGAAGTTTTCAGGCCTTCATCAA TTGATTTTGCCTCTTGGCCCTAAAGCCCCAAAATATTTTCCCGTCTGCCCGTTACGGAAA TTGATTTTGCCTCTTGGCTCTGAAAGCCCCAAAATATTTACCGTCTAGCCCCGTTACAGAAA AGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCTGTTGGATTATTAAAG TGATGCGTGGAGAAGGACTTTGAGCAGTGGCGGCGGCAGCAGCAGCGCCGGCCAGCTCAC AAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAG GTCCTGAGGAGCCCTGAGGTGGGCCAGGGGGCCAGGGGGAAGTTTTCAGGCCTTCATCAA S a

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524 TCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGCTAGTGGCCAG 465 548 GCTGCACCTGCCATCCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTGTCCTTAG 607 464 decrecaterecedererecederereceaerrradedecerteraerecertae 405 608 GAAGTAGCTCTGAGGCATGGGTTTTTCTGCTCCTGTGGGGCAGCTGGGGATAAGGTG 667 404 GAAGTAGCATGGAGGATTTTCTGCTCCTGTGCGGGCAGGCCAGCTGATGGATAAGGTG 488 TCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGCCAAGCTGCTGGCTAGTGGCCAG APPLICANT: Van 't Veer, Laura APPLICANT: Van 't Veer, Laura APPLICANT: Van de Vijver, Marc APPLICANT: Van de Vijver, Marc APPLICANT: Bernards, Rene TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients FILE REFERENCE: 9301-175-999 19.0%; Score 524; DB 15; Length 524; 100.0%; Pred. No. 1e-132; rative 0; Mismatches 0; Indels ( GAATATTATCTTTGAACCCAATGAAGTGTTTTTCTCCCCCATCAC 1011 н 44 GAATATTATCTTTGAACCCAATGAAGTGTTTTTCTCCCCCCATCAC CURRENT APPLICATION NUMBER: US/10/172,118 CURRENT FILING DATE: 2002-06-14 PRIOR APPLICATION NUMBER: 60/380,770 FRIOR FILING DATE: 2002-05-14 NUMBER OF SEQ ID NOS: 2699 SEQ ID NO 2364 FUBLICATION INFORMÀTION: DATABASE ACCESSION NUMBER: Contig46362 DATABASE ENTRY DATE: 2001-06-18 Sequence 2364, Application US/10172118 Publication No. US20030224374A1 Query Match 19.0% Best Local Similarity 100.0 Matches 524; Conservative APPLICANT: Dai, Hongyue APPLICANT: He, Yudong APPLICANT: Linsley, Peter APPLICANT: Mo, Mao APPLICANT: Roberts, Chris Homo sapiens GENERAL INFORMATION: RESULT 5 JS-10-172-118-2364/C US-10-172-118-2364 524 TYPE: DNA ORGANISM: 668 728 788 848 908 968 LENGTH: g  $\hat{o}$ g q q q q  $\mathcal{S}$ q  $\mathcal{S}$ g g 8 8 g  $\hat{o}$  $\delta$  $\delta$ 3 APPLICANT: Macing Roberto APPLICANT: Recipon, Herve APPLICANT: Recipon, Herve APPLICANT: Chen, Sei-Yu APPLICANT: Chen, Sei-Yu APPLICANT: Liu, Chenghua APPLICANT: Sun, Yongming APPLICANT: Sun, Compositions and Methods Relating to Lung Specific Genes and Prot FILE REFERENCE: DSV-0291 APPLICANTION NUMBER: US/09/989,920 CURRENT FILING DATE: 2001-11-21 CURRENT FILING DATE: 2001-11-21 SPRIOR APPLICATION NUMBER: 60/252,500 PRIOR FILING DATE: 2001-11-22 NUMBER: 07TWARE: Patentin version 3.1 ASEQ ID NO 99 1717 1897 2137 ŝ 1718 TCCAGCTGCTCCTTCCTGCTAAAAGGGGGACTGCTCACAGAGTGGCCTCAGCTTGGTGGTGTTTT 1777 1778 BAGGGGGCGCCCCCCCCCTCCATAAGGGTATCCTGGGCCCTGAGAATTCTGCCATCTGCC 1837 CTGTGGCCATCCAGCCCCTGTGGCTTGTCCAGCCTCTGCACCCCTGGTGTCTTCACT 1957 1958 CCAGGGGCAGACAGCAGCAGCAGCTGCAGTTCCTTCGTGAGTAACAGTAGCAGCAGCAG 2017 GATGGGGGCCAGGTCCCACA-GCTACTGATGGCCCGAGCTTGAGCTTCCTGGTGT 2196 2197 CCAGTCCGGAT-CCCACTTGCAGATCTCATGCTCAGATAGCTGGGACAAGTTCTTTTG 2255 280 520 640 41 GTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTG 100 160 220 580 401 CTGGGGCTAACAGGCTAGGCTTTGTGTTTGGTCAGCTTCAGCTCGATCCT 460 221 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGA 461 CCCTAAAGCAATGGGGAGGCCCCCACTAGCCCCAGTTTTCAGGAAGTCAACTGGGGAGGTTA 581 CCAGTCCGCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTG 1658 GTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCCATGTG 161 GAGGGGCCCCCCCCCCCCTTAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC 1838 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGG CCCTAAAGCAATGGGGGGGGCCCCCCCCACTAGCCCCAGTTTCCAGGAAGTCAACTGGGGAGGTTA Gaps 2256 TCACAGTGCTGG-CTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTC 2304 э; Length 960; Indels Aguery Match 22.2%; Score 612.4; DB 9; ABEst Local Similarity 99.4%; Pred. No. 8.4e-157; MAtches 646; Conservative 0; Mismatches 1; Sequence 99, Application US/09989920 Patent No. US20020172957A1 GENERAL INFORMATION: FEATURE: NAME/KEY: misc feature LOCATION: (716). (716) OTHER INFORMATION: a, c, g or t US-09-989-920-99 TYPE: DNA ORGANISM: Homo sapien -09-989-920-99 LENGTH: 960 1898 2078 + 2138 ( 2018 DĎ<sup>6</sup> 90 q Q δ q gD િ ઠે  $\delta_{i}$ Š 8 q d đ  $\mathcal{S}$ <u>q</u>  $\partial$ ð. 9  $\delta$ . <u>.</u> ų, ÷.

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GCCAAGGACGGTCAGTGCTTTGGGCCCAGGCCTGGCCGATGGGGGAAACCCAAACC 727

ATGTCCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGC 787 284 Arcrecedecedecedecedecededecededecederecerenteceretecededec 225

165 CCTCAGGTGGGCAGCAGGGGCCAGGGGGGGGGGAGTTTTCAGGCCTTCATCAAGAGGAACAACAT 847 corcaderecedencerterrereaseaserratedeservation 907 224 CCTGAGGTGGGCAGGGGGCCAGGGGGAGAGTTTTCAGGCCTTCATCAAGAGAAGAACAACAT

164 concademented accorrent concurrence active a GCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTATGATAGG 967

104 GCTAGCATACGGTGGGCCCACTGGCCCACTGGCTGTTTATGCCACTGATTATGATAGG 45

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US-10-074-475-1 Sequence 1, Application US/10074475 Publication No. US2003092898A1 Sequence 1, Application US/10074475 Publication No. US2003092898A1 APPLICANT Salead, Suama APPLICANT Macina, Roberto APPLICANT Recipon, Herve APPLICANT Recipon, Herve APPLICANT Salead, Subma APPLICANT Salead, Subma APPLICANT Salead, Subma APPLICANT Salead, Subma APPLICANT Salead, Subma APPLICANT Salead, Subma APPLICANT Cafferkey, Robert APPLICANT Cafferkey, Robert APPLICANT Cafferkey, Robert APPLICANT Cafferkey, Robert APPLICANT Cafferkey, Robert APPLICANT Cafferkey, Robert APPLICANT Cafferkey, Subma APPLICANT Cafferkey, Subma APPLICANT Sun, Yongmung APPLICANT Cafferkey, Subma APPLICANT Sun, Yongmung APPLICANT Cafferkey, Salead TITLE OF INVENTION CHERDING APPLICANT Sun, Yongmung APPLICANT Salead APPLICANT SALEAD	CTACAAAGGGGGCCTCACAGGCCTCAGGTTGGTGGTTTTTGAGGGGCCGCCCCCGG 17 [	QY     1795     CCCTCCATBAGGGTATCCTGGGGCTGAGAATTCTGCATTGGA-GGATGGACG     1853       DD     72     CCCTCCATBAGGGTATCCTGGGGCCTGAGAATTCTGCATTGGA-GGATGGACG     1853       DD     72     CCCTCCATBAGGGTATCCTGGGGCCTGAGAATTCTGCATTGGCATTGGATGGA	Qy       1854       CCTCAAATGGAAG-GAGTCCCACGGGAGATGGGTCCGAGGTCC-GGCTGTGGCCATCCAG       1911         Qy       1854       CCTCAAATGGAAG-GAGTCCCACGGGAGATGGGTCCGAGGTCCGAGGTCCGAGGCCATCCAG       1911         Db       132       CCTCAAATGGAAGGTCCCCAGGGAGATGGGAGGTCCGAGGTCCGAGGTCCGAGGCTCCAGGCCATCCAG       191	Qy         1912         CCCCCTGTGGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACG         1971           Db         1912         CCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACG         1971           Db         192         CCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACGS         251	QY 1972 CAGCCACTGCAGTTCCTTTCTCGTQAG-TAACAGTAGCAGCTGGGGGCTAACAG 2030 	Qy         2031         GCTAGGCTTTTGGTCGCGCATTTGGTCAGCTCTCCACTCGATCCTCCTAAAGCAATG         2090           Db         1	QY 2091 GGGAGGCCCCACTAGCCGAGTTTTCAGGAAGTCAACTGGGAGGGTTAGATGGGGGGCCAG- 2149 	Qy       2150       GGTCCCACAGGTAGATGGCCCGAGGCTGAGGTTCCTGGTGCGGGT       2207         Db	Qy         2208         CCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGGACAAGTTCTTTTGTCACAGTGCTGG         2267           Db         492         CCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGGACAAGTTCTTTTGTCACAGTGCTGG         551	QY         2268         CTCTGTCCTGAGGCCTCATTGCTGGCTGG         2296           Db         552         [	RESULT 8
RESULT 6 US-10-342-887-2364/C US-10-342-887-2364/C Sequence 2364, PpDitation US/10342887 Publication No. US20040058340Al APPLICANT: NPOWARTICN: APPLICANT: He, Yudoryus APPLICANT: He, Yudoryus APPLICANT: Mailey, Peter S. APPLICANT: None t' Veer S. APPLICANT: Senards, Sand Frognosis of Breast Cancer Patients TILE OF TIME OF TON NUMBER: 60/380,710 PRIOR APPLICATION NUMBER: 70,710 PRIOR APPLICATION NUMBER: 60/380,710 PRIOR APPLICATION NUMBER: 70,710 PRIOR APPLICATION NUMBER: 70,710 PRIOR APPLICATION NUMBER: 70,710 PRIOR APPLICATION NUMBER: 70,710 PRIOR APPLICATION NUM	Cuery Match Query Match Best Local Similarity 100.0%; Score 524; DB 16; Length 524; Best Local Similarity 100.0%; Pred. No. 1e-132; Matches 0; Gaps 0; Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy     48B     TCCCCCAATCTATGGGTCACAGGTAACAGATCTGAGGGGCAACTGCTGGCTAGTGGCCAG     547       Db     51     1 <t< td=""><td>Qy         548         GCCTGCCATCCCCGGCTTTAGGGCCTTTAGGGCCATCTAGAGGCAGTGCTTAG         607           Db         1</td><td>Qy         608         Gaagtagetreagegetreagegetreagegegegegegegegegegegegegegegegegegeg</td><td>Qy         668         GGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCGACGATGGGGAAAACCAAAACC         727           Db         111111111111111111111111111111111111</td><td>Qy         728         ATGTCCCCAGGGAAGGGCCAGAGGGCAGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGC         787           Db         284         ATGTCCCCCAGGGGAAGGGCCAGAGGGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGC         225</td><td>Qy     788     CCTGAGGFGGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACAT     847       Db     224     CCTGAGGTGGGGGGGGGGGGGGGGGGGGAGGTTTTCAGGCCTTCATCAAAGAGAACAACAT     165</td><td>QY     848     CCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGGTGTGGACTGCCCTTGTCA     907       D     1</td><td>QY         908         GCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTATGCTGATTATGATAGG         967           D         104         GCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTATGCCACTGATTATGATAGG         967</td><td>Qy     968     GAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCAC     1011       Db     1                                    </td><td>RESULT 7</td></t<>	Qy         548         GCCTGCCATCCCCGGCTTTAGGGCCTTTAGGGCCATCTAGAGGCAGTGCTTAG         607           Db         1	Qy         608         Gaagtagetreagegetreagegetreagegegegegegegegegegegegegegegegegegeg	Qy         668         GGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCGACGATGGGGAAAACCAAAACC         727           Db         111111111111111111111111111111111111	Qy         728         ATGTCCCCAGGGAAGGGCCAGAGGGCAGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGC         787           Db         284         ATGTCCCCCAGGGGAAGGGCCAGAGGGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGC         225	Qy     788     CCTGAGGFGGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACAT     847       Db     224     CCTGAGGTGGGGGGGGGGGGGGGGGGGGAGGTTTTCAGGCCTTCATCAAAGAGAACAACAT     165	QY     848     CCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGGTGTGGACTGCCCTTGTCA     907       D     1	QY         908         GCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTATGCTGATTATGATAGG         967           D         104         GCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTATGCCACTGATTATGATAGG         967	Qy     968     GAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCAC     1011       Db     1	RESULT 7

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1275 ÷, 1276 C-TTTTTTAAAAGAATAAAATGACTTGGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGAT 1334 1335 GAGCGGTTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTCGCTGGCGAGC 1394 1454 1455 GGGAATGCAGAGCCCTTTGCTTTCCTTGTTGCGGCCTGCTTCCTGTTCCTGGGGGACCCGC 1514 1515 TGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATGCGTGGAGAAGGACT 1574 248 CTTTTTTTAAAGAATAAAATGACTTGGTTTGGCTTGGAAGCAGGGGGAAGCATTCAGAT 128 368 308 68 9 CAGACCTCCATCCCCTGTTGGATTATTTAAGAAAGCCTCAGACAGTAAGGG 189 CCCCCTTGGAAGSTTCTGGTGCTTCAGCTGGCTGCTGCAGAGGTCCCGCCCCGGCTCGTGGT 1395 CCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTGCTGCAGAGTCCACCCGGCGTGGTGGT 249 GGGAATGCAGAGCCCTTTGCTTCCTTGCTGGCCTGCTTCCTGGGGGACCCGC Gaps ; ; ; APPLICANT: Dirkson, Mark APPLICANT: Dirkson, Mark APPLICANT: Labat, Ivan TITUE OF INVENTION: Lee Milliam TITUE OF INVENTION: Lee Milliam TITUE OF INVENTION: XVI CHILR REFERENCE: 2300-1652CON CURRENT FPLICATION NUMBER: US/10/609,021 CURRENT FPLICATION NUMBER: 00/192,583 CHRRENT FILING DATE: 2000-03-26 PERIOR FILING DATE: 2000-03-28 PERIOR FILING DATE: 2000-03-28 PERIOR FILING DATE: 2000-03-27 PERIOR FILING DATE: 2001-03-27 PERIOR PERIOR PERIOR FILING DATE: 2001-03-27 PERIOR Score 357.4; DB 16; Length 395; Pred. No. 4.2e-87; 0; Mismatches 11; Indels 1; TTGAGCAGTGGTGGGCAGCAGTGGCCT 1601 369 Treaccacrecteccaccaccaccri 395 Escobedo, Jaime Innis, Michael A. Garcia, Pablo Dominiguez Sudduth-Tinger, Julie Reinhard, Christoph Sequence 176, Application US/10609021 Publication No. US20040086913A1 GENERAL INFORMATION: Randazzo, Filippo Kennedy, Giulia C. Pot, David Kassam, Altaf 13.0%; 96.9%; APPLICANT: Williams, Lewis T. Lamson, George Drmanac, Radoje Dickson, Mark Query Match Best Local Similarity 96.9' Matches 375; Conservative UR ORGANISM: Homo sapiens US-10-609-021-176 He, Zhijun US-10-609-021-176 LENGTH: 395 1575 ' 69 APPLICANT: TYPE: DNA APPLICANT: APPLICANT: Thu Dec APPLICANT: APPLICANT: APPLICANT YO. qq ð a 8 q q qq 2 gQ  $\partial$  $\delta$ -

Sequence 90, Application US/09989920 Patent No. US20020172957A1 GENERAL INFORMATION: PAPLICANT: Macina, Roberto APPLICANT: Recipon, Herve APPLICANT: Recipon, Herve APPLICANT: Chen, Sei Yu APPLICANT: Chen, Sei Yu APPLICANT: Chen, Sei Yu APPLICANT: Sun, Yongming APPLICA ö 1903 GCCATCCAGCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGG 1962 ÷, 1723 CIGCICTICCTGCTACAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGG 1782 1783 GCCGCCCCCCCCCCTAAGGGTATCCTGCGCCTGAGAATTCTGCATCTGCCATTGG 1842 1843 AGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCGGAGGTCCGGCTGTG 1902 2381 CCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTCTAATGTTCATCTATTTAAAAT 2440 61 GCCCCCCCCCCCCTCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCGCCATTGG 120 121 AGGATGGACAGGCTCAAATGGAAGGAGTCCCACGGGAAGATGGGTCCGAGGTCCGGCTGTG 180 181 éccarécecérereresecriéresécéréresécéréségéreséréreségéreségés 240 CrectCrtCcrectAcAAAGeeGACrectCACAGTeeCCrCaGCTreGTerTreAGee 60 1963 GCCAGACAGCAGCCACTGCAGTTCCTTCCTTCGTGAGTAACAGTAGTGATAGCAG 2017 0; Gaps 241 GGCAGACAGCAGCACTGCAGTTCCTTCTTCGTGAGTAACAGTAGTGATAGCAG 295 Gaps 5; 8.1%; Score 224.4; DB 9; Length 251; 98.8%; Pred. No. 9.6e-51; 10.7%; Score 295; DB 15; Length 295; 100.0%; Pred. No. 4.6e-70; trive 0; Mismatches 0; Indels APPLICANT: SWITZEY, AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY FITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY FILLE REFERENCE: 210121.568 CURRENT APPLICATION NUMBER: US/10/116,712 CURRENT FILING DATE: 2002-04-07 CURRENT FILING DATE: 2002-04-07 SOFTWARE: FASTSEQ for Windows Version 4.0 1; Indels Pred. No. 9.6e-51; 0; Mismatches 1. APPLICANT: Bangur, Chaitanya S. APPLICANT: Switzer, Ann Publication No. US20030194764A1 Query Match 10.7% Best Local Similarity 100.0 Matches 295; Conservative Matches 237; Conservative TYPE: DNA ORGANISM: Homo sapiens TYPE: DNA ORGANISM: Homo sapien Query Match Best Local Similarity GENERAL INFORMATION: -920-90/0 US-10-116-712-429 US-09-989-920-90 SEQ ID NO 429 LENGTH: 295 251 SEQ ID NO 90 LENGTH: RESULT 10 US-09-989 qq đ 8 8 20 a q 8 8 g 3

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0y       2441       GATTTCTTTCTAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTCTAA       2500         191       131       131       132         0y       2501       131       132         0y       2501       131       132         0y       2561       36716667167676667666676766677666776367636	; LENUTH: 161 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-102-524-1276 Query Match 5.8%; Score 161; DB 15; Length 161; Rest Local Similarity 100.0%; Pred. No. 1.88-33; Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY       1727       TCTTCCTGCTACAAAGGGACTGCTCACGGGGGCCC       1786         Db       161       TCTTCCTGCTACAAAGGGGACTGCTCACGGGGCCC       1786         Db       161       TCTTCCTGCTACAAAGGGGACTGCTCACGGGGCCC       102         QY       1787       CCCCCCGGGCCCTCCAAGGGGCCTCAGGGCCTGAGGACGCG       102         QY       1787       CCCCCCGGGCCCTCCATAGGGGCCTGAGGACTTGCAATGGCGCGG       1846         Db       101       CCCCCCGGGCCCTCCATAGGGGCCTGAGGACTTGCAGGGCCTGAGGGG       42	Qy     1847     TGGACAGCCTCAAATGGAAGGAGTCGCGGGGGGAGATGGGTC     1887       Db     41     TGGACAGCCTCAAATGGAAGGAGTCCCCACGGGGGGGGGG	US-09-854-867-10 US-09-854-867-10 Sequence 10, Application US/09854867 Sequence 10, Application No. US2030224356A1 GENERAL INORMATION: GENERAL: INORMATION: APPLICANT: ADAN, KNOLL H APPLICANT: NORAN, PETER K TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING FILE REFERENCE: 30307	CURRENT FILING DATE: 2003-05-08 NUMBER OF SEQ ID NOS: 613 SOFTWARE: Patentin version 3.1 SEQ ID NO 10 TRNGTH: 2285	TYPE: DNA DRANTSM: Homo sapiens	: FEATURE: : NAME/KEY: repeat_region

MAR/KEY: misc\_feature COATTON: (377). (377) THER INFORMATION: n is a, c, g or t AME/KEY: misc feature OCATTON: (580) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (651). (651) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature COATTON: (654). (664) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (725) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (725). (725) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (725). (1095) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1257). (1151) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1251). (1151) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1251). (1151) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1251). (1351) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1351). (1351) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1351). (1351) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1365) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1365) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1365) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1365) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1365) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1365) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1365). THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1370) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1370) THER INFORMATION: n is a, c, g or t EATURE: MAR/KEY: misc feature OCATTON: (1365). (1351). Z/KEY: misc feature ATTON: (1990). (1990) BF INFORMATION: n is a, c, g or t 54-867-10 ч ų ц ц ц ц ч ч ч ч ч ч ų ч ATION: (1)..(2285) ER INFORMATION: cheshire FURE:

1017 AAAAATTCTTATTTTTAGTAGACATGTATTTTACCAAAAATATGTGTACTCAATTATTGTAT 1076 Match 3.4%; Score 93.6; DB 10; Length 2285; Local Similarity 67.3%; Pred. No. 2.5e-14; es 183; Conservative 1; Mismatches 70; Indels 18; Gaps

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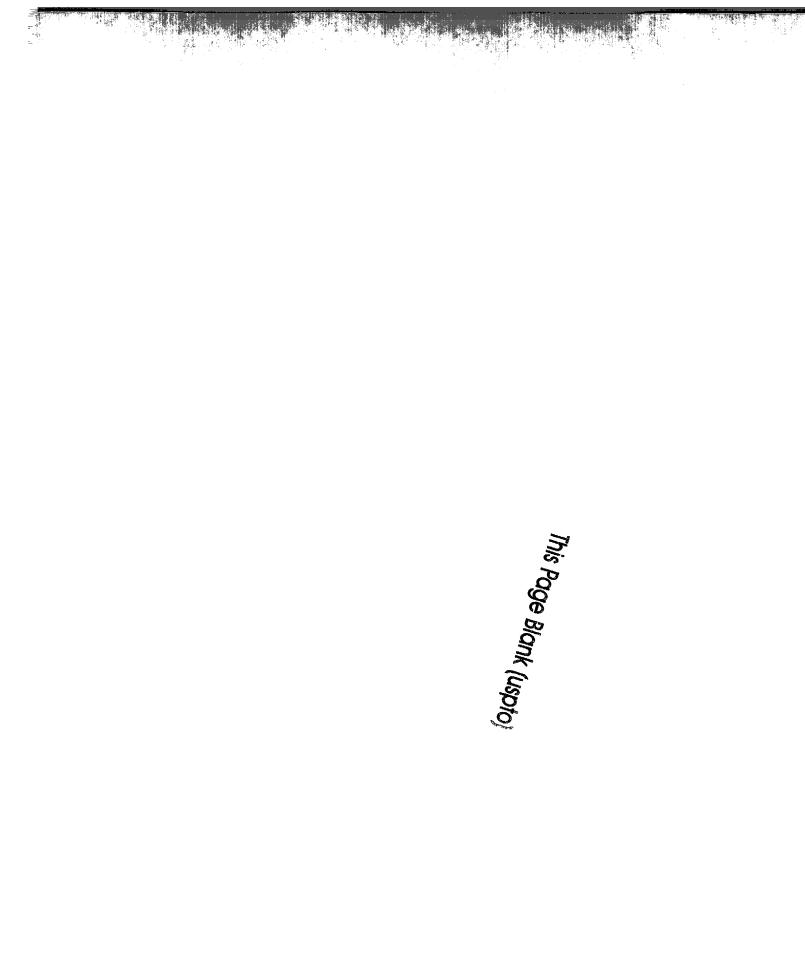
	RESULT 13 US-09-764-879-292/c Fequence 292, Application US/09764878 Fequence 292, Application US/09764878 Ference No. US20020090615A1 GENERAL INFORMATION: APPLICATIVE NORMATION: APPLICATION UNBER: US/09/764,878 FILE REFERENCE: PA121 CURRENT FILING DATA removed - consult PALM or file wrapper FILE REFERENCE: 2001-01-17 FILE REFERENCE: PA121 CURRENT FILING DATA removed - consult PALM or file wrapper FILE REFERENCE: 2001-01-17 FILE REFERENCE: 2001-01-17 FILE REFERENCE: PA121 FILE REFERENC	2.7%; Score 75; DB 9; Length 32038; larity 65.3%; Pred. No. 1.5e-08; Conservative 0; Mismatches 60; Indels 16; Gaps 2;	AATTATT         AATTATT	8 15-	gtatctačataacaátctcagttttacctcttagcccacaaagcctaaaatatttactat 28700 ctagcccgttacagaaaagtctgctgactactggccaggcc 1221 	RESULT 14 US-10-079-854-292/c US-10-079-854-292/c Sequence 292, Application US/10079854 Publication No. US2003054368A1 GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies FILE REFERENCE: PAI21C1 TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies FILE REFERENCE: PAI21C1 CURRENT FELLING DATE: 2002-02-22 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 428 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 292 TENGTH: 32038 TENGTH: 32038 TRPE: DNA ORGANISM: Homo sapiens
artccattcttct       artccattcttct       trtgaattttaccattcttct       tll       tll <td><pre>A-292/c B-292/supplication UFORMATION: US200209615P WFORMATION: US2002015P UFORMATION: Nucl INVENTION: Nucl INVENTION: Nucl SRENCE: PA121 APDLICATION NUME SRENCE: PA121 INVENTION UME SRENCE: PA121 INVENTION UME SRENCE: PA121 INVENTION CAL 2 20038 VA HOMO SAPIENTS VA HOMO SAPIENTS VA HOMO SAPIENTS</pre></td> <td>y Match Local Similarity 6 thes 147; Conservati</td> <td>AAAAAAATTT            AAATATTTAATTC Gwarterteattt</td> <td>GLATTITGGATTI GTTTTGATTI CAACAT</td> <td>gtatctačátaác ctagecegttacz             ctggeeerttatr</td> <td>54-292/c 592, Application on No. US2003005 NFORMATION: Nucl T: ROSEN et al. T: ROSEN et al. T: ROSEN et al. T: RUSEN PAI2ICI ERENCE: PAI2ICI ERENCE: PAI2ICI ERENCE: PAI2ICI ERENCE: PAI2ICI ERENCE: PAI2ICI FILING DATE: 20 plication remove FILING DATE: 20 plication Ver. Patentin Ver. 292 32038 M: Homo sapiens M: Homo sapiens</td>	<pre>A-292/c B-292/supplication UFORMATION: US200209615P WFORMATION: US2002015P UFORMATION: Nucl INVENTION: Nucl INVENTION: Nucl SRENCE: PA121 APDLICATION NUME SRENCE: PA121 INVENTION UME SRENCE: PA121 INVENTION UME SRENCE: PA121 INVENTION CAL 2 20038 VA HOMO SAPIENTS VA HOMO SAPIENTS VA HOMO SAPIENTS</pre>	y Match Local Similarity 6 thes 147; Conservati	AAAAAAATTT            AAATATTTAATTC Gwarterteattt	GLATTITGGATTI GTTTTGATTI CAACAT	gtatctačátaác ctagecegttacz             ctggeeerttatr	54-292/c 592, Application on No. US2003005 NFORMATION: Nucl T: ROSEN et al. T: ROSEN et al. T: ROSEN et al. T: RUSEN PAI2ICI ERENCE: PAI2ICI ERENCE: PAI2ICI ERENCE: PAI2ICI ERENCE: PAI2ICI ERENCE: PAI2ICI FILING DATE: 20 plication remove FILING DATE: 20 plication Ver. Patentin Ver. 292 32038 M: Homo sapiens M: Homo sapiens
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US-10-079-854-292 Query Match 2.7%; Score 75; DB 14; Length 32038; Best Local Similarity 65.9%; Pred. No. 1.5e-08; Matches 147; Conservative 0; Mismatches 60; Indels 16; Gaps 2;	1013 AAAAAAAAATTUTTATTAGTAGAGATGTATTTACCAAAAATATGTAGTAGTATTATT 107 	Qy 1073 GRATTTTGGATTTTATCATTTAAAAATTGTGGGAAATTTGTTTG	Qy     1126    CAACATAATATTGATTTGCCTCTTGGCTCTGAAAGCCCCAAATATTTACCGT     1178       Db     28759     GTATCTACATAATATCTCTCTTAGCCCCACAAAATATTTACTAT     28700	QY 1179 CTAGCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221 	RESULT 15 US-09-364-149 Sequence 498, Application US/09984429 Fequence 498, Application US/09984429 Fequence 498, Application US/09984429 TITLEART FROMMATION: 53 Human Secreted Proteins TITLE REFERENCE: P20182 CUREENT APPLICATION NUMBER: 05/09/984,429 FRIOR APPLICATION NUMBER: 05/09/984,429 PRIOR APPLICATION NUMBER: 05/09/984,429 PRIOR APPLICATION NUMBER: 05/01443 PRIOR FILING DATE: 2000-11-01 PRIOR FILING DATE: 2000-11-01 PRIOR FILING DATE: 2000-11-01 PRIOR FILING DATE: 09/288,143 PRIOR FILING DATE: 1997-10-09 PRIOR APPLICATION NUMBER: 06/061,529 PRIOR FILING DATE: 1997-10-09 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR FILING DATE: 1997-10-09 PRIOR PRIOR	Query Match 2.7%; Score 75; DB 11; Length 32844; Best Local Similarity 65.9%; Pred. No. 1.5e-08; Matches 147; Conservative 0; Mismatches 60; Indels 16; Gaps 2;	Qy     1013     AAAAAAAATTCTTATTTTTAGTAGACATGTATTTTCCCAAAAAATATGTACFCCAATTATT     1072       Db     3968     AAATATTTAATTCTTTTGTAGTAAGCCCGTATTACAAAAAAAA	Qy         1073         GTATTTTGGATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGC         1125           Db         4028         GTTTGAATTTTGCCAATAAAATTTCGTCCAAATTTTATTCTCTCTC	1
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4086 GTATCTACATAACAATCTCAGTTTTACCTCTTAGCCCACAAAGCCTAAAATATTTACTAT 4145

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: November 29, 2004, 08:42:07 ; Search time 1281 Seconds (without alignments)	Million cell upo taaaaagatgoggoo 8269772	ocessing	eeqn1358 eqn2338e seqn1358e seqn2000 seqn2000 seqn20002 seqn2002 seqn2002 seqn2002 seqn2002 seqn2002 seqn2002 seqn2002 seqn2002 sequ2000 sequ2000 sequ2000 sequ2000 sequ2000 s

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XX PI Salceda S, Macina RA, Hu P, Recipon H, Karra K, Cafferkey R; PI Sun Y, Liu C; XX DR WFI; 2002-657582/70 XX We breast specific nucleic acids and proteins, useful for identifying, PT diagnosing, monitoring, staging, imaging, and treating breast cancer and PT non-cancerous disease states in breast tissue, and in gene therapy. XX Claim 1; Page 148-150; 36700; English.	The present invention provides human breast specific coding proteins. These can be used in the diagnosis and treatment cancer and non-cancerous diseases of the breast. The presen a coding sequence of the invention Sequence 2754 BP; 557 A; 720 C; 753 G; 724 T; 0 U; 0 Other;	Query Match       100.0%; Score 2754; DB 6; Length 2754;         Best Local Similarity 100.0%; Pred. No. 0;       0; Indels 0; Gaps 0;         Matches 2754; Conservative 0; Mismatches 0; Indels 0; Gaps 0;       0; Indels 0; Gaps 0;         QY       1 GCCAGAAGCAGCCTCAGCTTGGCAAGGAGGAGGAGGAGGAGGAGGCAGTTGGG 60         Db       1 GCCAGAAGGAGCCTCAGGCTTGGCAAGGAGGAGGAGGAGGAGGAGGAGGCGCTGGGATTAGG 60         QY       61 GGCAAAAACAGGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGCCCCTGGCATTAGGAGGG         QY       61 GCCAAAAACAGGCCCCGGAGGAGGAGGAGGAGGAGGAGGCCCCTGGAATTAGG	<pre>61 GENERALGEGETCCCTGGGTAGCTAGCTGTTTTTCTTTTATCTTTTTGATCTTGTGTGA 61 GAGTGGATGGCTGCGGGGGGGGGGGGGGGGGGGGGGGGG</pre>	191       CCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGGTTCTCCCACAGGGTTCCCACAGGCA         181       CCCCAGAGCCAGGGCTTCTAGAGCGGGGTCTCCCCACATGACTGGCTTCACACAGGCA         241       CTTCCGCTCGGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGTAGGAAAT         241       CTTCCGCTCGGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGTTGCAGGTAGGAAAT         241       CTTCCGCTCGGGGTTGCATGCTTGTGTCTTACCGGTCCAGGGTTGCAGGTAGGAAAT         241       CTTCCGCTCGGGGTTGCATGCTCTGTGTCTTACCGGTCCAGGGTTGCAGGTAGGAAAT	Qy       301       GTTTGTACCTCTTTGTACGACCTTTGGGCCCCTTAGGGGCGTGGGGGGTTGGGGGGTTGGGGGGTTGGGGGGTTGGGGGG	<ul> <li>421 GAGAGCTCCTGAAACCCCCACTTAGCTTCCGAGACCTTTCTGCAAAAGCTCCTCCTGGCTT 48                                     </li></ul>	481 TCCTCCCTCCCCCAATCTATGGGTCCAGGTAACAGATCTGAGGGGAACTGCTGGTGGTGGTGGTAG 	rttagggccttctagaggcagtg 	stgcagggcagctgatggga 66	Oy       661       TAAGGTGGGGAAGGACGGTCAGTGGGCCCCAGCTGGCGCAGCATGGGGAAAA       720         Dy       661       TAAGGTGGGGAAGGACGGTCAGTGGGCCCCAGCTGGCCGAGCATGGGGAAAA       720         Db       661       TAAGGTGGGGAAGGACGGTCAGTCAGTGGTGGGCCCCAGCCTGGCGATGGGGAAAA       720	QV 721 CCAAACCATGTCCCCCAGGGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTGGTCCT 780
QY       2041       GTGTTCTGGGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC       2100         Db       2041       GTGTTCTGGGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC       2100         Db       2041       GTGTTCTGGGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC       2100         QY       2101       CATTAGCCCGGTTTGGGAAGTCAACTGGGGGGGGGGGGG	2221 CTCATGCTCTCAGATAGGTGGGGAAGTTCTTTTGTCACAGTGCTGGGCTCTGAGG 228 2221 CTCATGCTCTCAGATAGGTGGGGGGAAGTTCTTTTGTCACAGTGCTGGGCTCTGAGG 228 2221 CTCATGCTCTCAGATAGGTGGGGGGGGTCAGGTCTTTTTGTCACAGTGGCTGGGCTCGGGG 228 2281 CCTCATGCTGGCTGGGGTGGTGCTCTGCTGGGGAAAAAGCTTTGCGGGGGGCTTGCTT	2341       CacadaAdaGaGaArGFTFTGGGGFGCFCFCFGCAGCTCCCCGFGCTGGGFGGAA         2341       CacadaAgGGGAArGFTFTGGGGFGCFCFCFGCAGCTCCCCGFGCTGGGFGGAA         2341       CacadaAgGGGAArGFTFTGGGGGFGCFCFCFGCAGCTFCCFGCGGFGFGGAGGGAAGGGGGAAGGGGGACTGFTFTGGGGFGCFCFCFGCFGCFGCFGCFGCFGCFGGFGGFGGFG	QY         2461         ACCFOCAACACTTACGGAGAGACTATTATAGGAGGAGAGAGAGGAGAGACTCTCC         2520           Db         2461         ACCTCCAACACTTACCAGAATTGGGAGACTATTATAGGAGGAGATACTGGTC         2520           Db         2461         ACCTCCAACACTTACTCAGAATTGGGAGACTATTATAGGTGGAGGAGATACTGGTC         2520           QY         2521         GGGGTGGTGGGGCCTTGGATGGGTGGGGGTGGGGGGGGGG	QY       2581       TGAGCTCAAAGTTGTCCTACTGCCATGTTTTGTACCTGAAATAAAGCATATTTTGCACT       2640         Db       1	2701 TGCAAATAAAA              2701 TGCAAATAAAA 2	ABT07523 ID ABT07523 standard; cDNA; 2754 BP. XX AC ABT07523;	DT 14-NOV-2002 (first entry) XX DE Human breast cancer associated coding sequence SEQ ID NO: 2. XX	KW Human; breast specific gene; breast specific protein; breast cancer; XX gene therapy; cytostatic; gene; ss. XX Domo saviens	200	-FEB-2002; 2002WO-US00419	PR 13-FEB-2001; 2001US-0268292P. XX PA (DIAD-) DIADEXUS INC.

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Qy       1861       TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCGCCCTGTG       19         Db       1861       TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTCCAGCCCCCTGTG       19         Db       1861       TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGCGCCCCTGTG       19         Db       1961       TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCGCCCCTGTG       19         Qy       1921       GCTTGTCCACGGGGAGATGGCTCCGGGGTGGTCTTCACTCCCGGGGGCGAGCCACCTG       19         Db       1921       GCTTGTCCAGGCCCTGTGGCGCTCGTGGTGGTCTTCACTCCCGGGGGCCAGCCA	TGTTCTGGGGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC 	Db         2161 TACTGATGGCCGGGCCGGGTCGGGCTCCTGGGTGCCGGTCCCGCTTGCAGAT 22           Qy         2221 CTCATGCTCTCGGATAGGTGGGCACAGATCTTTTGTCAGGTGCTGGGCTCGGCTGGGGT 22           Qy         2221 CTCATGCTCCGGATAGGTGGGCACAGATCTTTTGTCACGGGCTCGGGCTCGGGG 22           Db         2221 CTCATGCTCCGGATAGGTGGGCACAGATCTTTTGTCACGGGCTCGGGCTCGGGC 22           Qy         2281 CTCATGCTGGCGGGGAAGGGCACAGATCTTTTGTCACGGGGGGCTTGGCTGGGGG 22           Db         2281 CCTCATTGCTGGCGGGGGGGGGGGGGGGGGGGGGGGGGCTGGCT	0y       2341       CACAGAAGAGAGAGAGCTGTTTGGGGTGCTCTTGCAGCTGCTGGGTGGAA       24         0y       2341       CACAGAAGAGAGAGAGTGTTTGGGGTGCTCTTGCAGCTCCCCGTGCTGGGTGGAA       24         0y       2401       GCAGGGTTACTGTGTTTTGGGGTGCTCTTGTGGGTGGGAAGGGGGGGG	2461         ACCTCCACACCTTTCCCAGATTGGGTGGACTCTTTTCTAAGGTGGGAGTATCTGTC         [	Qy       2581       TGAGCTCAAGGTTGTCCTACTGCCATGTTTTTGTACTGAATTAAAGGATATTTTGCACT       26         Db       2581       TGAGCTCAAGGTTGTCCTACTGCCAGGTTTTTGTACCTGAAATTAAAGGATATTTTGCACT       26         Db       2581       TGAGCTCAAGGTGCCACGCGCGAGGAGGTCTGGAAATTAAAGGATATTTTGGACT       26         Qy       2641       TGTTACTGAAGGTGGGGAGGGAGGGAGGCGTGGAAGGATTTTTGGACT       26         Db       2641       TGTTACTGTACGGGAGGGAGGCAGGGAAGGTCTGTGGGGTTAGGAA       27         Db       2641       TGTTACTGTACGCGGGGGGGAGGCAGGGAAGTCTGTGGGGGTTAGGAA       27         0y       2641       TGTTACTGTACGCGGGGGGGGAGGCAGGGAAGTCTGTGGGGTTAGGAA       27         0y       2701       TGCTAAATAAAGTCCCAATAGTGGGGAGGAAGGTCTGTGGGGGCC       2754	2701 TGCAAATAAACTCACATTTGTAAGAAAAAAAAAAAAAAA
CCAAACCATGTCCCCAGCGAAGGGCCAGAGTGGGGAACCTGTCCTCATGCCTTCGTCCT 78 GAGGAGCCCTGAGGTGGGGCGCGGGGGGCGGGGGGAGTTTTCAGGCCTTCATCAAGAGA 84 [1]	BCTGTTATC CTCCCCCATC CTCCCCCATC CTCCCCCATC CTCCCCCATC CTCCCCCATC STACTCCATT STACTCAATT	1081 GATTTPATCARTTAAAAATTGTGAAATTTGTTGCTCTTAGGCCAACATAATATTGAT 1140 1141 TTTGCCTCTTGGCTCTGAAAGGCCCAAAATATTTACCGTCTAGGCCGCAACAAAAAGTC 1200 1141 TTTGCCTCTTGGCTCTGAAAGGCCCAAAATATTTACCGTCTAGGCCGGTACAGAAAAGTC 1200 1201 TGCCTGCTGGGCTCTGGAGGCCCAAAATATTTACCGTCTAGGCCGGTTACAGAAAAGTC 1200 1201 TGCTGACTACTGGGCCCGGGCCCAAAATATTTACCGTCTGGCCGGTTACAGAAAAAGTC 1200	CTCAGACAGTAAGGGCTTTTTTTAAAAGAATAAAATGGCTGGTTGGGTAGGGCTGGGAGGGG 132 CTCAGACAGTAAGGGCTTTTTTTAAAAGAATAAAATGACTTGGGTTGGGTTGGAAGCAGG 132 CTCAGACAGTAAGGGGGGTTTTTTTAAAAGAATAAAATGACTTGGGTTGGGTTGGAAGCAGG 132 GGAAGCATTCAGATGAGGGGGGTTTTTTAAAAGAATAAAATGACTTGGGTTGGGTTGGAAGCAGG 138 GGAAGCATTCAGATGAGGGGGGTTTTTTAAAAGAATAAAATGACTTGGGTTGGGTTGGAAGCAGG 138 GGAAGCATTCAGATGAGGGGGGTTTTTTTAAAAGAATAAAATGACTTGGGTTGGGTTGGGAGGGGG 138	TGTGGCTGGGGGGGGGGGGCCCCCTTGGATTCTGGTGCTGGCTG	TCCTGGGGACCGCTGGGCCTTGGTCTGCATCCCCTGGGGTCGTGG         1           TCCTGGGGACCCGCTGGGCCTGGCCTGGCCTGGGGTCGTGGG         1           TCCTGGGGAGCCCGCTGGGCCTGGGCCTGGGCCGGGGCCGGGTTGATG         1           TCCTGGGGAGCCGCTGGGCCTGGGCCGGGGCGGGGCCGGGCTCGGGCTTGATG         1           TCCTGGGGAACCGCTGGGCCGGGGCGGGGCGGGCCGGCCCGCCC	1621       TGTCCTGGGGGGGGGGCGCTGATCTCACCTCCCCCTGGTAGAGGCCTT       1680         1621       TGTCCTGGGGGGGGGCGCTGATCTCACCTCCCCCTGGTAGAGGCCTT       1680         1621       TGTCCTGGGGGGCGCGCTGATCTCCCCCCTGGTAGCATCTGGGGACCTT       1680         1631       TGGCTTCTCGGGAGCCTGATCTCCCCCTGGTGGCGCTGCTGAGA       1740         1631       TGGCTTCTCGGAGGCCTCGCCCCCGGGGGCGCTGCTGCGGAGCTGACAA       1740         1631       TGGGTTCTCGGAGGCCTCGGAGGCTCTCCCCGGGGGGCGCTGCTGCAAA       1740         1741       AGGGGACTGCTGGAGGCCTCAGGTGGCTGCGGGGGCGCCCCCGGGCGCTCCCCGGGCGCTCCCCGGGCGCCCCCC

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<ul> <li>164. FRAMAGANGTCCACAGGAMAN FRANCESCACTAGAGCCACTAGAGCCACTAGAGCCACTAGAGCAGCACCACTAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC</li></ul>	92	86 86	040		16	16	22	28.28	46 6	r Ö	40	46	52	585	64 64	70						
1986 1986 1986 1986 1986 1986 1986 1986	1       TGGAAGGACTCCCACGGGAGATGGCT         1       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	I GCTTGFCCAGCCTCTGF3CACCCCGGGGGCGGGCGGCGGCGGCGGCGGCGGCGGCGGC	CAGETICCTTTCTFCGFGAGFAACAGTAGFGATAGCAGCTGGGGGCTAACAGGCTAACAGGCTAT     [	I GTGTTCTGCGCATTTGGCCAGCTTCTCACTCGATTGCGCGCAGGGGGGGG		CHTHEILINI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1 TACTGATGGCCCGGGGCTGGGTTGGGGCTGCTGGGGTGTCCGGGGTCCCGCTTGCAGAT 	1       CTCATGGTTGGGTGGGGACAAGTTCTTTTGTCAGGGTGGCTGGC		I CCLCAITECTESCIESCIESCIESCIESCIESCIESCIESCIESCIESCI	CACAGAAGAGAAGGGGACTGTTTTGGGGTGCCTCTCTGCTGCTGCGGTGGGTG	<pre>1 GCaCGGTTACTGTGTTCTCATGTTCTTGAAAGATTCTTTCTAAGATGTA                               </pre>	1         accrcacaccurrencegarreggerggergggergggggranden           1	I         GGGTGGTGGTCGTTGGATGGGTCGGGTGGGGTGGGGGGGG	TGAGCTCAAGCTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 	TGTTACTGTACCATAGTGCGGGCGGGGGGGGGGAGTCTGTGGGGATCTGGGTTGGA 	TGCAAATRAAACTCGCATTTGTAAGAAAAAAAAAAAAAAA	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	standard; cDNA; 2399 B		003 (first entry) 	cific nucleic acid (LSNA) #
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XW CALCEL MULLICITURY CALLET SCAPING, CALLET MAGAINY LUNG CALLET, XW non-cancerous diseases of the lung; transgenic animal; gene; 88.	n u	8
AA OS Homo sapiens.	0101	- 00
XX PN W0200268633-A2.		и 1 о
XX PD 06-SEP-2002.	ه م	
XX PF 21-NOV-2001; 2001W0-US043612.	7 10 7 10	1 -
XX PR 22-NOV-2000; 2000US-0252500P.		ALTATION MAGAGAMATATATATCH LUGACCOMATGMAGICALLACCCCCALLACACCATATA ALTATION (
XX PA (DIAD-) DIADEXUS INC.	7 1 U I	
XX PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;		
WPI; 2002-713376/77.	201 201	113
XX PT New isolated human nucleic acid molecule and polypeptide, useful for PT identifying, diagnosing, monitoring, staging, imaging and treating lung PT cancer and non-cancerne diseases of the lung	0 0	162
Claim 1; Page 238-240; 389pp; Englis	QY 1136 7	TIGATTITGCCTCTTGGCTCTGAAAGCCCCAAAATATTITACCGTCTGGCCGTTACAGAAA 1195 11/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1
	96TT 6T0T	1 11
	1559	
	QY 1256 2	AAAGCCTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAAGACTTGGTTTGGCTTGGAA 1315
	Db 1499 7	A A A A A A A A A A A A A A A A A A A
INVERTION, GENE THEREPY, PRODUCTION OF FIGURGENET ANNUALS OF of engineered lung tissue for treatment and research. This se encodes a lung specific nucleic acid	1316	GCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCAGCATCTCGTG 1375
	1439	3CAGGGGGAAGCATTCCAGATGAGGGGTTTCTGCATTAACCCTGCCTATCAGGGATGTCTGGG 1380 2002-2002-2002-2002-2002-2002-2002-20
uery Match 87.1%;	QY 1376 7 Db 1379 7	TCCTGTGTGGCTGGCGGCGCCCCCTTGGGAGGTTCTGGCTTCGGCTGGCT
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	Db 1319	Greekeeresteresteresteresteresteresteretteretteretteresteresteresterender 1260
	Qy 1496	CCTGTTCCTGGGGACCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGCT 1555
2339 ACCTGAGAGCTCCTGAAAACCCCCACTTAGCTTCCGGACCTTTTCTGCAAAAGCTCCTCCT	q	COTGTTCCTGGGGACCCCCTTGGGCCTTGCATCCCCTGGCCAGGTCCCTCAGGGT 1200
476 GGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGGGGGGAACTGCTGT 	000 000 000 000 000 000 000 000 000 00	Tearteediseasaasaasaatti taateediseeteediseeteediseasaatti tii 111111111111111111111111111111
Db 2279 GGCTTTCCTCCCTCCTCCTATCTATGGGTCACGGGCTAGGAGGGAG	. QY 1616	acteringrecendedagededecendenterenetereneterenenege         1675
2219 GCTAGGGCAGGGCTGCCAGCCAGCCATCCCCGGGTCTGCCACTTTAGGGCCTTCTAGAGG 2	Db 1139	ACTCTTGTCCTGGGGGGGGGGGGCCTGATCTCACCTCCACCTTGGGGACTGAGG 1080
596 CAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGCTTTTTCTGCTCTGTGCAGGGCAGCTGA	QY 16/6 Db 1079	ACTITICATION AND AND AND AND AND AND AND AND AND AN
Db 2159 CAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGCAG	QY 1736	TACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTGGTTTTGAGGGGGCCGCCCCCGGGC 1795
Db 2099 TGGGATAAGGTGGGGGAGGGGGGGGGGGGCGGGCCGGCCG		
	Db 959	CTCCCATAAGGGTAFCCTGGGGCCTGAGGAATTCTGCATTGGGAGGGAGGGAGGG
TTCATCAA	QY 1856	TCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCC 1915 1111111111111111111111111111111111
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Sequence 960 BP; 183 A; 351 C; 232 G; 193 T; 0 U; 1 Other; WO200268633-A2 06-SEP-2002 8 q 8 q 8 g S g  $\delta$ q S q δ qq 1975 2035 2095 2155 2215 2275 2335 2395 2515 2575 2455 2635 2695 720 660 600 540 180 780 480 420 360 300 240 179 GGCGTTGAGCTCCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAGCATATTTT 120 60 ч CACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGGCTAACAGGCTAAG TGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTTTTAAAATGGTTTCTTTTCTTAAGG CTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGC 839 CTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGGACAGCAGC GCTTTGTGTTTTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAG GCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGGCCAGGGTCCC 659 GCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGGGCCCAGGGTCCC ACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTG 599 ACAGCTACTGATGGCCCGAGCCAGGCTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTG 2216 CAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGGCTCTGTCC CAGATCTCATGCTCTCAGATAGGTGGGGGCCAAGTTCTTTTGTCACAGTGCTGGCTCTGTCC 2456 ATGTAACCTCCACACTTTCTCCAGATTGGGTGACTCTTTTCTAAGGTGGTGGGGGGGTAT GCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGT GCACTTGTTACTGTACCATAGTGCGGACGGACGAGAGAGTCTGTGTGGGATCTGGGGTCGGGACGAGGAGAGTCTGGGGT CACTGCAGTTCCTTTCGTGAGTAACAGTAGTGAGTAGTGGCGGCTAGCAGGCTAG 2576 GGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTT Lung specific nucleic acid (LSNA) #99 ВР CDNA; 960 (first entry) ABX92057 standard; 08-MAY-2003 2036 539 ( 2336 359 ' 2516 ( 1916 779 2096 2156 . 1976 719 2636 119 66 ABX92057 ABX92057 ID ABX RESULT qa ð qq 90 କୁସ å ò g  $\delta$ ð qq  $\delta$  $\delta$ qq q 5 â δ 8  $\mathcal{S}$ - ð  $\delta$ Db X \_\_\_\_\_ . . . . 1 ť -

identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. ö Liu 7 Sun Claim 1; Page 246; 389pp; English. s, Chen 21-NOV-2001; 2001WO-US043612. 22-NOV-2000; 2000US-0252500P Recipon H, (DIAD-) DIADEXUS INC WPI; 2002-713376/77. RA, Macina

of 120 10-1333 residue amin occid sequences (31), given in the specification, comprising any of 164 179-12421 base pair sequences (32), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence encodes a lung specific nucleic acid The invention describes an isolated human nucleic acid (I) encoding any

ik.

1837 с, 1777 1897 1957 2017 2137 1717 2077 280 520 160 220 340 400 460 41 GTACCTTGGGGACTGAGGACCTTTTGGCTTCTCGGAGCCTGCAAGCCTCTTCCCATGTG 100 GTACCTTGGGGACTGGGGACCTTTTGGCTTCTCTGGGGGCCTGCAGCCTCTTCCCÄTGTG TCCAGCTGCTCCTCCTGCTACAAAGGGGACTGCTCCACAGTGGCCCCCAGCTTGGTGGTTTT 221 ATTGGAGGATGGACCACCCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGGGGTCCGGG Crereaccarccadececcrerescreterccadecrrerecadecarcreter GAGGGGCCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC 1838 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGG CCAGGGGGCAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGGTAGCAG CCAGGGGCAGGCAGCCACTGCAGTTCCTTCTTCGTGAGTAACAGTAGTGATAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTAGCAGTAGCAG CTGGGGCTAACGGCTAGGCTTTGTGTGCGCATTTGGTCAGCTTCTCACTCGATCCT 461 CCCTAAAGCAATGGGGGGGGGCCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTA TCCAGCTGCTCCTTCCTGCTACAAAGGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTGGTTTT GAGGGGCGCCCCCGGGCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC creegecraacagecrassecrrrererrerececarrregreagerreacreacreatecr CCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGGAGGTTA Gaps з; Query Match22.2%;Score 612.4;DB 6;Length 960;Best Local Similarity99.4%;Pred. No. 1e-156;Matches646;Conservative0;Mismatches1;Indels3 1718 101 1778 161 1898 1958 1658 2018 2078 341 401 8 å

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GATGGGGGCCGGGGTCCCCA-GCTACTGATGSCCCGGGCCGGGTTGGGCTTCCTGGTGT

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Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal; gene; ss.

Homo sapiens

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qq	521 GATGGGGGCCAGGGTCCCACATGCTGCTGGTGGCCCGAGGTTGAGCTTCCTGGTGT 580	
ò	2197 CCAGTTCCGGAT-CCCACTTGCAGATCTCATGCTCTCAAGATGGTGGGGGACAAGTTCTTTTG 2255	
qq	581 CCAGTCCGGATCCCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTG 640	
yo qu	2256 TCACAGTGCTGG-CTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTC 2304	
2		
RESU ABV5 ID	LT 5 4530 ABV54530 standard; cDNA; 611 BP.	
XXX	ABV54530;	
2日3	17-SEP-2002 (first entry)	
S E S	Human prostate expression marker cDNA 54521.	
XXX	Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.	
XS	Homo sapiens.	
Y N I	W0200160860-A2.	
283	23-AUG-2001.	
PF V	20-FEB-2001; 2001WO-US005171.	
22 77 77 77 77	17-FEB-2000; 2000US-0183319P. 16-MAR-2000; 2000US-0188862P. 25-MAY-2000; 2000US-0207454P.	
면 지	-JUL-2000; -JUL-2000; -DEC-2000;	
YAX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
Z I Z	Schlegel R, · Endege WO, Monahan JB;	
S S S S	WPI; 2001-662795/76.	
PT Pr PT Pr PT Pr For	Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.	
S A X	Claim 1; Page 10539-10540; 11750pp; English.	
888	The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether	
888	a pattent is arritored with prostate cancer; (b) monitoring the progression of prostate cancer in a pattent; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing	
ខ្លួនទ	the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcingenic potential of a compound; (g)	
ខ្លួនខ្ល	determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker	
SQ	Sequence 611 BP; 111 A; 174 C; 164 G; 159 T; 0 U; 3 Other;	
A B C	Query Match 20.1%; Score 554; DB 5; Length 611; Best Local Similarity 99.5%; Pred. No. 7.8e-141; Matches 565; Conservative 0; Mismatches 2; Indels 1; Gaps 1;	
ço da	1194 AAAGFCTGGTGGCTACTGGGCCGGGCCTCCTTACCTCCCTGTGGATTATTTAA 1253 	

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WO200172781 - 42	man; ss; lung cancer; adenoc ostate cancer; benign prosta	Human cancer related cDNA sequence #176.	16-JAN-2002 (first entry)	AAS59058;	SULT 7 59058 AASS9058 standard; CDNA; 395 BP.	2268 CTCTGTCGTGAGGCCTCATTGCTGGCTGG 2296 	492 CCCACTTGCAGATCTCATGCTCAGATAGGTGGGGGGCAAAGTTCTTTTGTCACAGTGCTGG 551	2208 CCCACTTGCAGATCTCATGCTCCAGATAGGTGGGGACAAGTTCTTTGTCACAGTGCTGG	2150 GGTCCCACAGGTACTGATGGCCCGGAGCCAGGTTGAGCTT CCTGGTGTCCAGTCCGGGT 2207 	2031 GCTAGGCTTTGGTTCTGCGCATTTGGTCGCCTTCTCCTCGTCGTAAGCAATG 2090 	1972 CAGCCACTGCAGTTCCTTTCCTGAG-TAACAGTAATGAGGCTGGGGCTAACAG 203 	1912 CCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCGGGC	1854         CCTCAAATGGAAG-GAGTCCCAGGGAGAATGGGAGGAGGACCCAGGGTCCAGG         191           1854         [	1795 CCCTCCATAAGGGTATCCTGGGCCTGAGATTCTGCATCGCCATTGGA-GGATGGACAG 1853 		The present invention provides buman breast spectations: These can be used in the diagnosis. proteins. These can be used in the diagnosis is a coding sequence of the invention Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 Securestrative 97:54; Pred. No. 1:3e-1; 201 [][[][][][][][][][][][][][][][][][]][][]	lat ULL Control of the second s
		<pre>man; ss; lung cancer; adenocarcinoma; breast cancer; colon canc ostate cancer; benign prostatic hypertrophy; BHP; cytostatic.</pre>	<pre>man cancer related cDNA sequence #176. man; ss; lung cancer; adenocarcinoma; breast cancer; colon canc ostate cancer; benign prostatic hypertrophy; BHP; cytostatic.</pre>	-JAN-2002 (first entry) man cancer related cDNA sequence #176. man; ss; lung cancer; adenocarcinoma; breast cancer; colon canc ostate cancer; benign prostatic hypertrophy; BHP; cytostatic.	S59058; :JAN-2002 (first entry) man cancer related cDNA sequence #176. man: ss; lung cancer; adenocarcinoma; breast cancer; colon canc ostate cancer; benign prostatic hypertrophy; BHP; cytostatic.	7 6 S59058 standard; cDNA; 395 BP. S59058; -JAN-2002 (first entry) man cancer related cDNA sequence #176. man sacilung cancer; adenocarcinoma; breast cancer; colon canc ostate cancer; benign prostatic hypertrophy; BHP; cytostatic.	<pre>2268 CTCTGTCCTGAGGCCTCATTGCTGGGCTGG 2296 111111111111111111111 552 CTCTGTCCTGAGGCCTCATTGCTGGGCGGG 580 6 6 6 6 559058 standard; cDNA; 395 BP. 559058 standard; cDNA; 395 BP. 559058; -JAN-2002 (first entry) man cancer related cDNA sequence #176. man cancer related cDNA sequence #176. man s s: lung cancer; adenocarcinoma; breast cancer; colon cancostate cancer; benign prostatic hypertrophy; BHP; cytostatic.</pre>	<pre>7 2268 CTCTCTCTCATGCTCCATGCTCCAGATAGGTGGGGACAAGTTCTTTTGFCCACAGTGGCGG 2268 CTCTCTCTCTCGAGGCCTCATGCTGGCTGGGCTGGGGGGGG</pre>	<pre>2208 CCCACTTGCAGATCTCAGGTCGGAGAAGTTCTTTGTCAGGGGGGGAGAGTTCTTTGTCAGGGTGGG 492 CCCACTTGCAGATCTCATGGTCTCAGATAGGTGGGGAGAGTTCTTTTGTCACAGTGGTGG 2268 CTCTGTCGTGGGCCTCATGGTGGGGGGGGAGAGTTCTTTGFCACAGTGGTGG 2268 CTCTGTCCTGAGGCCTCATTGCTGGGGGGG 2296 11111111111111111111111111111111111</pre>	<pre>2091 GGGAGGCCCCACTAGCCAGTTTTCAGGAGGTTAGTTGGAGGGGTTAGTTGGGGGGGG</pre>	<pre>2031 GCTAGGCTTTGTGTTGGTCGGCTTTGGTCGGCTTGGTCGGTTGTT</pre>	<pre>1972 CAGCGACTCGATTCCTTTCTTCGTGAG -TAACAGTAGTGATAGCGGGGGGGGGGGGGGGGGGGGGGG</pre>	<pre>1912 CCCCCTGGGGCTTGTCCAGCCCTCGGGGCGGGGGGGGGG</pre>	<pre>1854 CCTCAAATGGAAG -GAGTCCCAGGGAGATGGGTCCGAGGTCC -GGCTGGGCCATCGAG 132 CCTCAAATGGAAG -GAGTCCCAGGGAGATGGTGGGTGGGCTGGGGCTGGGCCATCGAG 132 CCCCCTAATGGGATGGTCCAGGGAGATGGTCCGGGGGTGGGGGGGG</pre>		Ω.	S
<pre>2150 GGTCCCACAGCTACTGATGGCCCGAGCCAGGCTAGCTTCCTGGTGTCCGGAT 432 GGTCCCACAGCTACTGATGGCCCGAGCCAGGCTAGGCTTTCCTGGATGTCCAGTCCGGAT 432 GGTCCCAGGTCTCAGGTCGGATAGGTGGGCTTCCTGGATGTCCTTGTCCAGTGCGGGT 432 CCCACTTGGCGATCTCATGCTCGGATAGGTGGGACAGTTCTTTGTCCAGTGCGGGG 432 CCCACTTGGGGATCTCATGCTCGGATAGGTGGGACAGTTCTTTGTCACAGTGCGGGG 2268 CTCTGGCGGAGTCTCAGGTGGGACAGGTTCTTTGTCACAGTGCTGG 2268 CTCTGTCGGGGGATCTCAGGTGGGACAGGTTCTTTGTCACAGTGCTGG 2268 CTCTGCTCGGGGGTCGG 2296 1                                    </pre>	2150 GGTCCCACAGCTACTGATGGCCCGAGGCTGAGGCTT - CCTGGTGTCGGGTT 432 GGTCCCACAGCTACTGATGGCCCGAGGCTGGGGTTGGCTTTCCTGGATCCGGGTT 432 GGTCCCACAGCTCTATGGCCCGAGGCCGAGGCTTTCCTGGATCGGGTCGGGTT 2208 CCCACTTGGAGGTCTCATGGTCGGTGGGGGACAAGTTCTTTTGTCACAGTGCGGG 492 CCCACTTGGAGGCCTCATGGCTGGGTGGGGGGACAAGTTCTTTTGTCACAGTGCGGG 2268 CTCCTCGGGGGCTCATTGGCTGGGTGG 2296 111111111111111111111111111111111111	2150       GGTCCCACAGCTACTGATGGCCCGAGCCGGGTTGAGCTT - CCTGGTGTCGGGTTCGGGTTGAGGCTTCCGGTTCGGTTCGGGTTCGGGTTCGGTTCGGGTTC	2150       GGTCCCACAGCTACTGATGGCCCGAGCCGGGTTGAGCTT - CCTGGTGTCCGGTCGGGTT         432       [	2150       GGTCCCACAGCTACTGATGGCCCGAGCCAGGCTTGAGCTT - CCTGGTGTCGGGTCGGGT         432       [	2150       GGTCCCACAGGTACTGATGGCCCGAGCCAGGTTGAGCTT CCTGGTGCGGTTCGGGTT         432       GGTCCCACAGGTACTGATGGCCCGAGCCAGGTTGAGCTTTC-CGGTCCGGAT         432       GGTCCCACAGGTACTGATGGCCCGAGCTAGGCTTTCCTGGATGTCCGGTTCCGGAT         2208       CCCACTTGCAGTTCATGCTCACGTAGGCGGGGACAAGGTTTCTTGGGATGTCCGGAT         2208       CCCACTTGCAGTTGCTCACGATGGCGGGGACAAGGTTCTTTGTCACGGTGCGGAT         2208       CCCACTTGCAGATCCATGCTCTCAGATGGTGGGGGACAAGGTTCTTTGTCACAGTGCGGATGG         492       CCCACTTGCAGGTTGCTGGTGGGGAGCAAGGTTCTTTTGTCACAGTGCTGG         2268       CTCTGTCCTGAGGCCTCATGCTGGCTGG       2296         111111111111111111111111111111111111	2150 GGTCCCACAGCTACTGATGGCCCGAGCCTGAGCTTCCTGGTGTCCAGTCGGGT 1111111111111111111111111111111111	2150 GGTCCCACAGGTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGCCGGTT 	2150         GGTCCCACAGCTAGTGGCCCGAGCCAGGCTTGGGCTT CCTGGTGCCGGTCCGGGT           2110			2031 GCTAGGCTTT5IGTTCTGCGCATTTGGCCGCTCTCCGCGCATCCCCCCTAAGGCATG 	1972       CAGCCACTGCAGTTCCTTTCTTCGTGGG-TAACAG         1072       1011111111111111111111111111111111111	<ul> <li>1912 CCCCCTGTGGGCTTGTCCGGCCTCTGGCCCCCGGGGGCGGGCGGGGGG</li></ul>	1854 CCTCAAATGGAAG-GAGTCCCAGGGGAGATGGGTCC-GGCTGTGGCCATCCAG [1][1][1][1][1][1][1][1][1][1][1][1][1][	214 431		0
<pre>1795 cccrccontradeGGTWTCCTGGGCCTGGGAWTTCTGGATTCTGCATTGGATTGAUTUAU 72 ccrcCaAAGGGAWTCTGGGCCTGGGGAWTTCTGGATTCTGCATTGGATTGAUTUAU 1854 ccrtCAAATGGGAWGTGAGCCTGGGGAGGATTCGGATCGGACTGGGCCAACGGG 1854 ccrtCAAATGGGAWGTGAGCTCTGGGAGGATGGGATGGGACGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG</pre>	<pre>1795 cccrcorrandoscrarcerrandom reconstrated and an analysis and and and any analysis and and and and and and and and and and</pre>	<pre>1795 CCCTCCATAAGGGTATCCTGGGCCTGGAATTCTGCATTGGA-GGTTGGAATGGAA</pre>	<ul> <li>1795 CCCTCCATAAGGGTTATCTGGGGCTGGGATTTGGATTGGGATTGGATGGA</li></ul>	<ul> <li>1795 CCCTCCATAAGGGTTATCCTGGGCCTGAGANTTCTGCATCTGCATTGGAFGGAFGGAFGGAFGGAFGGAFGGAFGGAFGGAFG</li></ul>	<ul> <li>1795 CCCTCCATAAGGGTATCCTGGGCCTGAGATTCTGCATTCGCATTGGCATTGGCATGGGTATCCCCCTTACAGG</li> <li>1814 CCCCCATAGGGTATCCTGGGCTGGGTATCTGCATTGGCATTGGCATTGGCATGGGTAGGGTATCGGGTATGGGAGTGGGTAGGGTAGGGTAGGGTAGGGTAGGGTAGGGTAGGGTAGGGTAGGGCATGGGAGTGGGCATGGGAGTGGGCATGGGAGTGGCATGGGAGTGGGTAGGGCATGGGGAGTGGCATGGGAGTGGCATGGGGAGGGCAGGGGTGGGGTGGGCAGGGGTGGGGTGGGCAGGGGCAGGGGGGGG</li></ul>	<ul> <li>1795 CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATTGGCATTGGCATGGGATGGGTATCCTGGGTATCGGGTATCCTGCGTTGGCATTGGCATTGGCATTGGCATGGAAGGGTATCCTGCGTATGGGAATTCTGCATTGGCATTGGCATGGGAGGGGGAGGGGGGGG</li></ul>	<ul> <li>1795 CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATTGCATTGGA-GGATGGACGGTATCTGCATTGGATGAGGTATCCTGGGCATTGCATGAGGTATCTGCATTGGATGAGGTATCCTGGGATAGGGATTCTGCATTGAATTCTGCATTGGATGAGGATGGGATCGGGATCGGGATCGGGATGGGATGGGATGGGATGGGATCGGATCGGATCGGAGAATCGGAGAATCGGAGATCGGAGATCGGAGATCGGAGATCGGAGAATCGGAGAATCGGAGATCGGAGATCGGAGATCGGAGATCGGAGAAGAAGAATGGAATGGAGAATCGGAGAATCGGAGAATCGGAGAAGAGAAGAGAAGAATCGGAGAAGAAGAATCGGAGAAGAGAAGAATCGGAGAAGAGAGAG</li></ul>	1795 CCCTCCATAAGGTATCCTGGGCCTGAGAATTCTGCATTGGCATTGGCATGGCAGGGCAGGGCAGGGTATCCTGGGCATTGGGCATTGGCATTGGGATGGGTAGGGTATCCTGGGTATGGGGTATCGGGCATTGGGATGGGAAGGGTAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGG	<pre>1795 CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATTGCATTGGCATTGGA GGATGGAGA 72 CCCTCCATAAGGGTATCCTGGGCTGGGGAATTCTGCATTGGCATTGGA GGATGGAG 1854 CCTCCAAATGGAAG GAGTCCGGGGGAATTCTGCATTGGCATTGGCATTGCAG 132 CCTCCAAATGGAAG GAGTCCCGGGGGAGATGGGATCGCCATTGGCATTGCAG 132 CCTCAAATGGAAG GAGTCCCAGGGGAGATGGGATCGCCATGGCATTGCAG 132 CCTCAAATGGAAGTCGCCCGGGGGAGATGGGATCGCGGGGTCGGGCCATCCAG 132 CCTCAAATGGAAGTCGCCCCGGGGGAGATGGGATCGCGCGGGGGGGG</pre>	1795       CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCATTGGA - GGATGGACAG 185         72       CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATTGGA - GGATGGACAG 185         1854       CCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATTGGA - GGATGGACAG 185         1854       CCTCCATAAGGGGTATCCTGGGCCATCGGGCCATTGGA - GGATGGACAG 131         1854       CCTCCAAATGGAAG - GGATGCCCGGGGCCATCGGGCCATCGAG 131         1854       CCTCCAAATGGAAG - GGATGGGCCCAGGGGCCATCGAGGCCATCCAG 131         1852       CCTCCAAATGGAAG - GGATGGGCCCGGGGGAGGAGGCCAATCGAG 131         1912       CCCCCGGGGGCAGGGGGGAGAAGGGGCCCGGGGGCCGGGGCCAACCAG 137         1912       CCCCCGGGGGCTGGGCCCCGGGGGGGGGGGGGGGGGGG	1795       CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCATTGGA-GGATGGACAG       185         72       CCTTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATTGGATGGA	1795       CCCTCCATAAGGSTATCCT3GGCCT3GGAATTCTGCATCTGCATTGGA-GGATGGACAG       185         72       CCCTCCATAAGGSTATCCT3GGCCT3GGAATTCTGCATTCGCATTGGATGGATGTATCGA       131         73       CCCTCCATAAGGSTATCCT3GGGCCT3GGAATTCTGCATTCGCATTGGATGGATGTATCGA       131         185       CCCTCCATAAGGSTATCCT3GGGGCGGGGGGGGGGGGGGCTGCGGGCATGCAG       131         185       CCTCCAATGGAAG-GAGTCGGGGGGGGGGGGGGGGGGGGCGGCGGCCATCCAG       191         132       CCTCAAATGGAAGGTGGGTCCCGGGGAGAATGGGCTCCAGGGCTGGGCGGGGGGGG	195 CCCTCCATAAGGSTATCCTGGGCCTGGGAATTCTGCATCTGCATGGA-GGATGGACAG 185 		179. 71		
<pre>1735 CTACAAAGGGGACTCCCACAGTGGCCCTCACTTGGTGGTTTTTGAGGGCCGCCCCCG 1735 CCCTCCACTAAGGGGTATCCTGGGGTTGGCATTTGAGGGCCGCCCCCCG 1735 CCCTCCACTAAGGGGTATCCTGGGGATGGGATTTGGCATTGGCATTGGCATTGGGATGGGATGGGATGTGGGATGGAGAGGAAGTGGAAGGAGGGG</pre>	<pre>1735 CTACAMAGGGGATGCTCAAGTGGCTCAGCTTGGCTTGGCGATTTTGAGGGCCCCCCCC</pre>	<pre>1735 CTACAMAGGGACTCCTACAGTGGCTCAGCTGGTGGTGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGT</pre>	<pre>1735 CTACAMAGGGACTCCTACAGTGGCCTCAGGTGGTGGTTTTTTAGGGGCCCCCCCC</pre>	<ul> <li>1735 CTACAMAGGGGATTGCTCACAGTGGCTCAGCTTGGTTTTTTTTTT</li></ul>	<ul> <li>1735 CTACAAAGGGGACTGCTCAGGTGGCTTGGTGGTTGTTGGACTTGGGGCTCGGGGTGGCTCGGGCTCGGGTTGGTGGTTGGTTTGAGGGCCCCCCGGG CTACAAAGGGGGTATCCTGGGCTCAGGTGGCTTGGTTTTGAGGGCCCCCCCGG CTACAAGGGGGTATCCTGGGCTCGGGGCTCGGGGGCTGGGGCCCCCCCGG CCCCCATAAGGGGTATCCTGGGCTCGGGGGTCGGGGCTGGGGCTCGGGGTCGAGGT CCCCCATAAGGGTTCCTGGGCCTGGGGGTCGGGGTCGGGGTCGGGGTGGGGTTGGAG 132 CCCCAAATGGAAG-GAGTCGCGGGGGAGGTGGGGTCGAGGGTCGAGGGTCCAGG 1932 CCCCAAATGGAAG-GAGTCGCGGGGGGGGGGGGGGGGGGG</li></ul>	<ul> <li>1735 CTACAAAGGGGACTGCTCAGTGGCCTCAGTTGGCGGTTTTTGAGGGGCCCCCCCG CTACAAAGGGGACTGCTCAGTGGCCTCAGTTGGTGGTTTTTGAGGGGCCCGCCC</li></ul>	<ul> <li>1735 CTACAAAGGGGACTGCTCAGTGGCCTCAGTGGCTTGGTGGTTTTGAGGGGCGCGCCCCGG CTACAAAGGGGACTGCTCAGTGGCCTCAGCTTGGTGTTTTGAGGGGCCGCCCCGG CTACAAAGGGGTATCCTGGGCCTGAGTTGGTGTTTGGCATTGAGGGGCCCCCCGG CCTCCATAAGGGTATCCTGGGCCTGGGACTTGGCATTGGAGTGGGGCCCCCCGG CCCCCTGTGAGGGTATCCTGGGCCTGGGAATTCTGCATTGGCATTGGAGGCCCCCCGG 1795 CCCCCATAAGGGTATCCTGGGCCTGGGAATTCTGCATTGGCATTGGAGGCCCCCCGG 132 CCTCCAAATGGAAG-GAGTCCTGGGCCTGGGGCTCGGGGGTGGGGGCGAGCAG 132 CCTCCAAATGGAAG-GAGTCCCGGGGGGGGGGGGGGGGGG</li></ul>	<ul> <li>1735 CTACAAAGGGGACTGCTCAGTGGCCTCAGTGGCTTGGTGGTTTTTGAGGGGCGCCCCCGG CTACAAAGGGGGACTGCTCAGTGGCCTCAGCTTGGTGTTTTTGAGGGGCCCCCCGG CTACAAAGGGGGACTGCTCAGGTGGCCTGAGTTGGTGTTTTTGAGGGGCCCCCCGGG CTACAAAGGGGTATCCTGGGCCTGAGGTTGGTGTTTTGAGGGGCCCCCCGGG CCCCCCTGTAAGGGTTTCTTGGGCCTGAGGTTCGGCATTGGA - GGATGGGCCCCCCGG CCCCCCTGTAAGGGTTTCTTGGGGCCTGAGGGTCCGAGGGTCC-GGCTGGGGGCCATCCAG 1854 CCTCCAAATGGAAG-GGGCCCGGGGGAGATTCTGCCTCGCCATTGGCATTGGAG-GGATGGAAGG 11                               </li></ul>	<ul> <li>1735 CTACAAAGGGGACTGCTCAGTGGCCTCAGTGGTGGTTTTGAGGGGCGCCCCCGG</li> <li>1795 CTACAAAGGGGACTGCTCACGGTGGCCTCAGTTGTTGGTGGTTTTGAGGGGCCCCCCGGG</li> <li>1795 CCTCCAAAGGGGACTGCTCAGGGCCTGAGAATTCTGCATCTGCATTGAGGGCCCCCCCGG</li> <li>1795 CCTCCAAATGGAAG GGCTCCAGGGCGTGAGAATTCTGCATTGGCATTGGAGGGCCCCCCGGG</li> <li>1854 CCTCAAATGGAAG GGCTCCAGGGGCGTGAGAATTCTGCATTGGCATTGGAGGGCTCAGG</li> <li>1854 CCTCAAATGGAAG GGCTCCCAGGGGGAGAATTCTGCATTGGCATTGGAGGGCTCAGG</li> <li>1854 CCTCAAATGGAAG GGCTCCAGGGGGCTGGGGGCTCCGCGGGGGGCATAGGGAGGCTCCCGGGGGGGG</li></ul>	<ul> <li>1735 CTACAAGGGGGACTGCTCACAGTGGCCTCAGCTGGTGGTGTTTGGGGGGCGCCCCCCGG 179</li> <li>1795 [[                                   </li></ul>	1735       CTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGCGTTGGGGGCGCCCCCCGG       179         12       CTACAAAGGGGACTGCTCAGTGGCCTCAGGTGGTTTTGAGGGGCCGCCCCCGG       71         13       CTACAAAGGGGACTGCCAGGTGGCCTCAGGTGGCTTTTGAGGGGCCGCCCCCGG       71         1795       CCCTCCATAAGGGTATCCTGAGTGGCCTCAGGTGGCTTTTGGAGTGGACGGCCCCCCGG       131         1795       CCCTCCATAAGGGTATCCTGAGTGGCCTGAGAATTCTGCATTGGCATTGGAGGGAG	<pre>1735 CTACAAAGGGGACTGCTCACAGTGGCCCTCAGCTTGGGGGCGCGCCCCCGG 179 12 [                                    </pre>	1735       CTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTGTTTGAGGGGCCCCCCCG       179         111111111111111111111111111111111111	1735         CTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGCGCCCCCCGG         179.           111111111111111111111111111111111111	6; Length 591; 21; 7; Indels 7; Gaps	17.6%; Score 483.8; D 97.5%; Pred. No. 1.3e- vative 0; Mismatches	Query Mato Best Loca Matches
<pre>March march march model m</pre>	<pre>Match int 17.6% Seede 40: 3, 9 D5 i length 591; actches 55; Conservative 0; Mismatches 7; Indels 7; Gaps 173 GracoAAGGGGATGCTCAGGTGGCTCAGGTGGTGGTGTTTTAGGGGCCCCCCCC</pre>	<pre>Match. 17.6% Secore 493.3, DB 5, Length 591, matches 55; Connervative 0, Mismatches 7; Indels 7, Gaps 173 Charlestyr 97.5% Pread 173 Charlestyr 97.5% Pread 173 Charlestyr 97.5% Pread 173 Charlestyr 97.5% Pread 173 Charlestyr 97.5% Pread 174 Charlestyr 97.5% Pread 175 Charlestyr 97.5% Pread 185 Charlestyr 97.5% Pread 192 Charlestyr 97.5% Pread 193 Charlestyr 97.5% Pread 194 Charlestyr 97.5% Pread 195 Charlestyr 97.5% P</pre>	<pre>Natch. 17.6% Score 433 J; DB 5; Length 591; Active 555; Conservative 0; Mismaches 7; Indels 7; Gaps 1735 CTACAAAGGGAACTGCTAAGTGGGCTTAGGTGGATTTTAAGGGCCGCCCCGG 1735 CTACAAAGGGAACTGCTCAAGTGGCTTAGGTGGATTTTAAGGGCCGCCCCGG 1735 CTTCAAAGGGAACTGCTCAAGTGGCTTAGGTGGATTTTAAGGGCCGCCCCGG 1735 CTTCAAAGGGAACTGCTCAAGTGGCTTAGGTGGATTTTAAGGGCCGCCCCGG 1735 CCTCCAAAGGGAACTGCTCAAGGTGGCATTTGAGGGCCGTCCCGG 1735 CCTCCAAAGGGAACTGCTCAGGGCAATTGGCATTGGGCGATTGGAGGATTCCCCCCCC</pre>	<pre>Natch. 17.6% Score 433 % DB 6; Length 591; hest Local Similarity 77.5% Fred. No. 1.3 = 121; list TroAMAGGGAACTGCTAAGTGGCCTCAGCTGGTGGTGGTTTTGAGGGGCGGGC</pre>	<pre>NMECH 17.61; Score 403.9; DB 5; Length 591; Actober 555; Cranservative 0; Mismatches 7; Irdels 7; Gaps 1735 Cranservative 0; Mismatches 7; Irdels 7; Gaps 1932 Creticanadescritercondecoradametricacturedarandametric 1932 Creticanadescritercondecoradametricacturedarandametric 1932 Creticanadescritercondecoradametricacturedarandametric 1932 Creticanadescritercondecoradametricacturedarandametric 1932 Creticanadescritercondecoradoradescritercondecoradorades 1932 Creticanadescritercondecoradoradescritercondecoradorades 1932 Creticanadescritercondecoradoradescritercondecoradorades 1932 Creticanadescritercondecoradoradescritercondecoradorades 1932 Creticanadescritercondecoradoradescritercondecoradorades 1932 Creticanadescritercondecoradoradescritercondecoradorades 1933 Creticanadescritercondecoradoradescritercondecoradorades 1933 Garadescritercondecoradoradescritercondecoradorades 1933 Garadescritercondecoradoradescritercondecoradorades 1933 Garadescritercondecoradoradescritercondecoradorades 1933 Garadescritercondecoradoradescritercondecoradorades 1933 Garadescritercondecoradoradescritercondecoradorades 1933 Garadescritercondecoradoradescritercondecoradorades 1934 Mismatchestercondecoradoradescritercondecoradorades 1935 Garadescritercondecoradoradescritercondecoradorades 1936 Garadescritercondecoradoradescritercondecoradorades 1937 Garadescritercondecoradoradescritercondecoradorades 1938 Garadescritercondecoradoradescritercondecoradorades 1939 Garadescriterenterco</pre>	<pre>bury Match bury M</pre>	<pre>buery Match buery Match buery Match 17.64; Score 483.8; DB 6; Length 591; lest Local Similarity 97.34; Pred. No. 1.38-121; lest Local Similarity 101101101101101101101101101101101101101</pre>	<pre>buery Match 17.6%; Score 483.8; DB 6; Length 591; lest Local Similarity 97.5%; Pred. No. 1.3e-121; lest Local Similarity 10.00000000000000000000000000000000000</pre>	<pre>buery Match 17.6%; Score 483.8; DB 6; Length 591; set Local Similarity 97.5%; Pred. No. 1.3e-121; lest Local Similarity 10; line line line line line line line line</pre>	<pre>buery Match 17.6%; Score 483.8; DB 6; Length 591; atches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 6 1735 CransadeGGGACTGCACGAGGGCCTGGACGTGGGGGCGCGCCCCCGG 179 [                                    </pre>	<pre>buery Match 17.6%; Score 483.8, DB 6; Length 591; sest Local Similarity 97.5%; Pred. No. 1.3e-121; latches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 6 1735 cracAadeGGGACGCTCAGTGGCTTGGCTTGGGGTTGTGGGGGGGCGCCCCCGG 71 12 CTAAAGGGGGACGCTCAGTGGCCTGGGTTGGTGGTTTTGAGGGCCGCCCCCGG 71 13 cracAadeGGGTATCCTCAGTGGCCTGGGTTGGTGGTTTTGGGGGCCGCCCCCGG 71 13 cccrcCaTaAGGGTATCCTGGGTGGGTGGTGGTGGTTTGGGGCGCCCCCCGG 71 13 cccrcCaTaAGGGTATCCTGGGTGGGTTGGTGGTTTGGGGCGTTGGGA GGATGGGGCCCCCCCGG 71 13 cccrcCaTaAGGGTATCCTGGGCTGGGCTTGGGTGTTTGGGGCGTTGGGA GGATGGGGCCCCCCCGG 71 13 cccrcCaTaAGGGTATCCTGGGCTGGGGCTGGGGTGTTGGGGGCGTTGGGA GGATGGGGCCTGCGG 71 13 cccrcCaTaAGGGTATCCTGGGCTGGGGGTGGGGGCGTTGGGA GGATGTGGGGCGTGGGGGCGTGGGGCGTGGGGGCGTGGGGCGTGGGGGCGTGGGGCGGC</pre>	Duery Match         17.6%         Score 483.8%         DB 6;         Length 591;           Best Local Similarity         97.5%;         Pred. No. 1.3e-121;         7;         Gaps         6           Iatches         555;         Conservative         0;         Mismatches         7;         Indels         7;         Gaps         6           1735         Canservative         0;         Mismatches         7;         Japs         6           1735         Canservative         0;         Mismatches         7;         Japs         6           1735         Cancecracadeoscracacraceccracacarregosccacccccccccccccccccccccccccccccccccc	<pre>buery Match 17.6%; Score 483.8; DB 6; Length 591; sest Local Similarity 97.5%; Pred. No. 1.3e-121; latches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 6 1735 CTACAAAGGGGACTACACATAGCCCTAGGCTTGGTGTTTTGAGGGGCGCCCCCCGG 179                                     </pre>	<pre>buery Match 17.6%; Score 483.8% DB 6% Length 591% sett Local similarity 97.5%; Pred. No. 1.3e-121% latches 555% Conservative 0% Mismatches 7% Indels 7% Gaps 6 1735 CTACAAAGGGGACTGCTCACAGTGGCCCTCAGGTGGTGGTGGTGGCGGGGGGGG</pre>	0 U; 0 Other	591 BP; 106 A; 166 C; 172 G; 147 T;	
<pre>Sequence 51 B7, 106 Å, 166 C, 173 G, 147 T, 0 U, 0 Ocher; WerY Match Metch S55; Conservative 0; Mismatches 7; Indels 7; Gaps 1735 FTARAMAGGABATTOTATTGGCTAGGTTGGTGGTGGTGGGGCGCGCCCCC 1735 FTARAMAGGABATTOTACTAGGTCTAGGTTGGTGGTGGTGGGGGGGGCGCCCCCCCC</pre>	<pre>Sequence 531 BP; 106 Å; 166 C; 173 G; 147 T; 0 U; 0 Other; March as islarity 7: %; scree 403 as D \$6; Length 591; atches 555; conservative 0; Mismatches 7; Indels 7; Gaps 1735 CrACAMAGGGANCTCCACACACACACACACACACACACACACACACACAC</pre>	<pre>Sequence 591 BP; 106 A; 166 C; 173 C; 147 T; 0 U; 0 other; merry Match sequence 555; Conservative 0; Mismatches 121; Indels 7; Gaps 173 Gracomacgeoarcreative 0; Mismatches 7; Indels 7; Gaps 173 Gracomacgeoarcreatewartive 0; Mismatches 7; Indels 7; Gaps 173 Gracomacgeoarcreatewarterchanderreatemandant 2 CHUMMINTHININIIIIIIIIIIIIIIIIIIIIIIIIIIIIII</pre>	<pre>Sequence 591 BP; 106 A; 166 C; 173 C; 147 T; 0 U; 0 other; mery Match. 175 Grantaryty 97:5%; 5core 403 3; DB 6; Length 591; merches 25; Connervative 0; Miamaches 7; Indels 7; Gaps 179 Cinternational (11). 171 Cinternational (11). 179 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 172 Cinternational (11). 173 Cinternational (11). 173 Cinternational (11). 174 Cinternational (11). 174 Cinternational (11). 175 Cinternational (11). 175 Cinternational (11). 175 Cinternational (11). 175 Cinternational (11). 176 Cinternational (11). 177 Cinternational (11). 177 Cinternational (11). 178 Cinternational (11). 178 Cinternational (11). 178 Cinternational (11). 179 Cinternational (11). 179 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 172 Cinternational (11). 173 Cinternational (11). 174 Cinternational (11). 175 Cinternational (11). 176 Cinternational (11). 177 Cinternational (11). 177 Cinternational (11). 178 Cinternational (11). 178 Cinternational (11). 178 Cinternational (11). 179 Cinternational (11). 170 Cinternational (11). 170 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 171 Cinternational (11). 172 Cinternational (11). 173 Cinternational (11). 173 Cinternational (11). 174 Cinternational (11). 175 Cinternational (11). 177 Cinternational (11). 178 Cintern</pre>	<pre>sequence 531 BP, 106 A, 166 C, 173 G, 147 T, 0 U, 0 Other; wery Match atches 552. Conservative 0; Mismatches 7; Indels 7; Gaps atches 552. Conservative 0; Mismatches 7; Indels 7; Gaps 1735 CTACAMAGGGAACTCCTACAGTGGCCTCAGGTGGCTTTGAGGGGCCGCCCCG 1735 CTACAMAGGGAACTCCTCAGAGTGGCCTCAGGTGGTTTTTAGGGGGCCGCCCCGG 1735 CTACAMAGGGAACTCCTCAGAGTGGCCTCAGGTGGTTTTTTAGGGGGCCGCCCCGG 1735 CCCCCATAGGGGAACTCCTCAGGGGGGAAATTCTGGCATTGGAGGGGCGCCCCCGG 1735 CCCCCATAGGGGAACTCCTCAGGGGGGAAATTCTGGCATTGGAGGGGGGGG</pre>	<pre>sequence 591 BP; 106 Å; 166 C; 172 G; 147 T; 0 U; 0 other; mery Match 17.64; Score 403.9; DB 6; Length 591; atches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 1735 CTACAMAGGGGACTCCCAGGTGGGCCTCAGGTTGGGTTTTGAGGGGCCCCCCCG 1735 CTACAMAGGGGACTCCTCAGGTGGGCTTGGGTTTTGAGGGGCCCCCCCG 1735 CTACAMAGGGGACTCCTCAGGTGGGCTTGGGTTTTGAGGGCCCCCCCC</pre>	<pre>sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 U; 0 Other; buery Match 17.6%; Score 483.8; DB 6; Length 591; atches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 1735 CracAAAGGGGACTGCTCAGAGGGGCTCAGCTTGGTGTTTTTGAGGGGCCGGCC</pre>	<pre>Sequence 591 BP, 106 A, 166 C, 172 G, 147 T, 0 U, 0 other; bery Match 17.6%; Score 483.8; DB 6; Length 591; est Local Similarity 97.5%; Pred. No. 1.3e-121; latches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 1735 CTACAMAGGGAACTGCTCACAGTGGCCTCAGGTTATGAGGGGCCCCCCCGG CTACAMAGGGAACTGCTCACAGTGGCCTCAGGTTATGAGGGCCCCCCCGG 1795 CTACAMAGGGAACTGCTCACAGTGGCCTCAGGTTATGAGGGCCCCCCCGG 1795 CCCTCATAAGGGTATCCTGGGCCTCAGGTTGGGGCTTTGAGGGCCCCCCCGG 1795 CCCTCATAAGGGTATCCTGGGCCTCAGGTTGGGGCTTTGAGGGCCCCCCGGG 1795 CCCTCAATGGGATTCCTGGGGCTGGGGGCGAGGGGGGGGG</pre>	<pre>Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 U; 0 Other; best Local Similarity 97.5%; Pred. No. 1.3e-121; hatches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 173 Conservative 0; Mismatches 7; Indels 7; Gaps 1795 CcrrccarpagedacrecreaAgregecreaderarrandegedecrecede 1795 CcrrccarpagedacrecreaAgregecreaderarrandegedecrecede 1795 Ccrrccarpagedacrecreadedarrandegregrintandegedecrecede 1795 Ccrrccarpagedacrecreadedarrandegregrintandegedecrecede 1795 Ccrrccarpagedacrecreadedarrandegederarrandegedecrecede 1795 Ccrrccarpagedacrecreadedarrandegederadegedecrecede 1795 Ccrrccarpagedacrecreadedarrandegederadegedecreceded 1795 Ccrrccarpagedacrecreadedarrandegederadegedecreceded 1795 Ccrrccarpagedacrecededacredgearrandegederadegedecreceded 1795 Ccrrccarpagedacredgearrandegederadegederadegedecreceded 1795 Ccrrccarpagedacredgearrandegederadegederadegedecreceded 1912 Cll[1][1][1][1][1][1][1][1][1][1][1][1][1][</pre>	<pre>Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 U; 0 Other; bery Match 17.6%; Score 489.3; DB 6; Length 591; est Local Similarity 97.5%; Pred. No. 1.3e-121; latches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 1735 CTACAAGGGGACTCCTCAAGTGGCCTCAAGTTGGTTTTAAGGGCCCCCCCC</pre>	<pre>Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 U; 0 Other; buery Match 17.6%; Score 483.8; DB 6; Length 591; atches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 6 1735 CracAaAaccoderectcacarredecreacerragerectrarreacecceccecce 179 L2 CTACAAAaccoderectcacarreacercradearreacercaccarreacerccecce 179 L2 CTACAAAaccoderectcacarreacercradearreacerreacecceccecce 185 1795 Ccrecaraacedearreacercradearreacerreacerreacercecce 185 1795 Ccrecaraacedearreacercradearreacercradearreacercecce 185 1795 Ccrecaraacedearreacercradearreacercradearreacercece 185 1795 Ccrecaraacedearreacercradearreacercradearreacerced 185 1795 Ccrecaraacedearreacercradearreacercradearreacerecece 185 1795 Ccrecaraacedearreacercradearreacercradearreacereced 185 1795 Ccrecaraacedearreacercradearreacercradearreacereced 191 1854 Ccrecaraacedeareacercradearreacercradearreacereced 191 1854 Ccrecaraacedeareacercradearreacercradearreacerecedearreace 1854 Ccrecaraacedeareacercradearreacercradearreacerecedearea 191 1854 Ccrecaraacedeareacercradearreacercradearreacerecedearea 191 192 Ccrecaraacedeareacercradearreacerecedeareaceredeareacedea 191 192 Ccrecaraecerreacercradeareacerecedeareacerecedeareaceredeareacerea 1972 Cadecarreacererecedeareareacercradeareareacereace</pre>	<pre>Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 U; 0 Other; bery Match 17.6%; Score 483.8, DB 6; Length 591; set Local Similarity 97.5%; Pred. No. 1.3e-121; latches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 6 1735 CTACAAAGGGGACTGCAGTGGCCCTCAGCTTGGGGTGTTTTGAGGGGCCGCCCCCGG 179 12 CTACAAAGGGGACTGCAGTGGCCCTCAGCTGGGTGGTTTTGAGGGGCGGCCCCCCGG 71 12 CTACAAAGGGGACTGCAGTGGCCCTGAGAATTCTGCATTGGAGGGGCGGCCCCCCGG 71 1795 CCCTCATAAGGGGTAGCCTGAGGGCCTGAGAATTCTGCATTGGAGGGCGGCCCCCCGG 71 1795 CCCTCATAAGGGGTATCCTGGGCCTGAGAATTCTGCATTGGATGGA</pre>	<pre>Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 U; 0 Other; buery Match 17.6%; Score 483.8, DB 6; Length 591; set Local Similarity 97.5%; Pred. No. 1.3e-121; latches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 6 1735 CTACAAAGGGGACTGCAGTGGCCCTCAGGTGGGTGTTTTGAGGGGCCGCCCCGG 71 12 CTACAAAGGGGACTGCAGTGGCCCTCAGGTGGGTGTTTTGAGGGGCGGCCCCCCGG 71 1795 CCCCATAAGGGGACTGCAGTGGCCTGGGTGGGTGTTTTGAGGGGCGGCCCCCCGG 71 1795 CCCCATAAGGGGACTGCAGTGGCCTGGGTGGGTGGTTTTGGAGGGGCGGCCCCCCGG 71 1795 CCCCATAAGGGGACTGCAGGGCCTGGGGTGGGTGGTTTTGGAGGGCGGCCCCCCGG 71 1795 CCCCCATAAGGGGTAACCTGGGCGTGGGTGGGTGGTTTTGGAGGGCGGGC</pre>	Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 U; 0 Other; buery Match 17.6%; Score 483.8, DB 6; Length 591; ast Local Similarity 97.5%; Pred. No. 1.3e-121; latches 555; Conservative 0; Mismatches 7; Indels 7; Gaps 6 1735; Craczaaocococrecacracorrescorreagermogracerrrreageococcocccccc 179; 1735; Craczaaocococrecacracorrescorreagermogracerrrreageococccccccc 77; 1735; Craczaaocococrecacracorrescorreagermogracerrrreageoccccccccc 77; 1735; Craczaaocococrecacracorrescorreagermogracerrrreageoccccccccc 71; 12; Craczaaocococrecacorrescorreageorreagerergeneerrreageocccccccccccc 71; 1795; Creccaraadeorscreageocreageorreagermogracerreagered 185; 1795; Cccrccaraadeorarterreageocreageorreageneerrancecccccccccccccccccccccccccccccc	Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 U; 0 Other;           Duery Match         17.6%; Score 483.8; DB 6; Length 591;           Dest Local Similarity         97.5%; Pred. No. 1.3e-121;           Iatches 555; Conservative         0; Mismatches         7; Gaps         6           1735         CTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTGGTGGGGGGGG	and treatment of breast st. The present sequence	diseases of the bre invention	CC proteir CC cancer XX a codir

Ä 1454 GGGAATGCAGAGCCCTTTGCTTTCCTTGCCGCCTGCTTCCTGTGCGGGACCCGC 1514 The invention relates to an isolated polynucleotide comprising a nucleotide sequence which hybridises to a sequence selected from one of set fully defined sequences jiven in the specification, antiense molecules complimentary to the sequences, the polypeptides encoded by the sequences and antibodies raised against the proteins. The nucleic acids are useful for detecting differentially expressed genes which correlate with a cancerous state of a mammalian cell i.e. diagnosing cancer and deencearcinomal. Modifying the gene products of the mucleic acids adenocarcinomal. Modifying the gene products of of the mucleic acids in gene mapping and tisue profiling. The present sequence is one of the 316 cancer related CDMA sequences 1276 C-TTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGGAAGCATTCAGAT 1334 1335 GAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCGAGC 1394 128 248 308 309 TGGGCCTTTGGTCTGCATGCCCTGGCCAGGTCCCTCAGGGCCTGATGCGCGCGTAGAAGGACT 368 68 Ĥ 69 CTTTTTTTTAAAAGGAATAAAATGACTTGCGTTTGCGCTTGGAAGCAGGGGAAGGATTCAGAT 189 ¢¢¢¢¢TTĠĠāAĠĠTT¢TĠĠTĠĊTTĊAĠĊTĠĠĊŦĊĊTĠĊAĠAĠŦĊĊAĊĊĊĊĠĊĊĊŦĊĠŦĠĠŦ 249 GGGAATGCAGAGGCCCTTTGCTTTCCTTGCCGCCCGCCTGCTTCCTGGGGACCCGC CCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTGCTGCAGAGTCCACCCCGCCTCGTGGT Labat 1; Gaps Sudduth-Klinger J; New human polynucleotides useful for the treatment and diagnosis of Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinge Reinhard C, He Z, Randazzo F, Kennedy GC, Pot D, Kasam A; Lameon G, Drmanac R, Czkvenjakov R, Dickson M, Drmanac S, I Leshkowitz D, Gizveijakov V, Ones LW, Stache-Crain B; Length 395; Sequence 395 BP; 70 A; 111 C; 109 G; 105 T; 0 U; 0 Other; 11; Indels 13.0%; Score 357.4; DB 4; 96.9%; Pred. No. 4.4e-87; tive 0; Mismatches 11; TTGAGCAGTGGGCGGCAGCAGTGGCCT 1601 369 rreadcadredredredcadcarredrer 395 Claim 1; Page 202; 240pp; English. ЧH 28-MAR-2000; 2000US-0192583P. ADD49697 standard; cDNA; 295 Query Match 13.0 Best Local Similarity 96.9 Matches 375; Conservative (CHIR ) CHIRCN CURP. (HYSE-) HYSEQ INC. WPI; 2001-626251/72. 1395 1455 1575 ADD49697; cancer. RESULT 8 ADD49697 ID ADD4 XX ADD4 AC ADD4 XX I5-J qq  $\mathcal{S}$  $\mathcal{S}$ g 8 g 8 qq  $\mathcal{S}$ qq q  $\delta$ 8 q

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Human lung cancer associated cDNA 61594667.	O'm	Query Match Best Local S
Human; ss; lung cancer antigen; cytostatic; lung cancer; gene therapy; vaccine; T-cell; tumour.	Σ	Des
Homo sapiens.	5 7	1725
US2003194764-Å1.		
16-OCT-2003.	δο 	58/T
04-APR-2002; 2002US-00116712.	90 J	61
05-APR-2001; 2001US-0282289P. 05-OCT-2001; 2001US-0327511P.	87 A	121
(CORI-) CORIXA CORP.	δλ ι	1903
Bangur CS, Switzer A;	ସ୍ପ	181
WPI; 2003-844452/78.	δ	1963
New isolated polypeptides and polynucleotides useful for diagnosing, preventing and treating cancer, particularly lung cancer.	qu	241
Claim 1; SEQ ID NO 429; 250pp; English. The invention relates to an isolated polynucleotide (a) comprising any of	ABX	RESULT 9 ABX92048/c ID ABX92048
quèncés appearing as ADD49269 - mulements of (a): sequences of at	XX AC	ABX92048
	X LO	08-MAY-20
ants of (a). Also included ar ig: sequences encoded by the r	XX DE	Lung spec
polynucleotide; any of the 4 amino acid sequences fully defined in the specification; or sequences having at least 70 or 90% identity to the	XX KM	Human; ge
sequence in (a) or $(\tilde{b})$ ), an expression vector comprising the above polynucleotide operably linked to an expression control sequence, a host	KW KW	
čeli transformed or transfected with the above expression vector, an isolated antibodv. or its antigen-binding fragment, that specifically	XX SO	Homo sapi
binds to the above polypeptide, an oligonuclectide that hybridises to the above-mentioned nucleotide sequences under highly stringent conditions, a	XX MA	
fusion protein comprising at least one polypeptide cited above, detecting the presence of a cancer in a patient (comprising: obtaining a biological	XX	06-SEP-2(
sample from the patient; contacting the biological sample with a binding	XX	
agent that binds to the polypeptide, or with the oligonucleotide cited above; detecting in the sample an amount of the polypeptide that binds to	XX	72-AON-12
the binding agent, or an amount of a polynucleotide that nypridies to the oligonucleotide, and comparing the amount of polypeptide, or	XX	17 - AON - 77
polynucleotide that hybridises to the oligonucleotide, to a predetermined cut-off value and then determining the presence of a cancer in the	PA XX	(DIAD-) 1
patient), a method for stimulating and/or expanding T-cells specific for a tumour propein (comprision contacting T-cells with the above	Iđ	Macina R <i>1</i>
polypeptide, polynucleotide or antigen-presenting cells that express the	ND Y	WPI; 2002
reprinting the second of the second of a time state of the second second of the second	5 II II II	New isola identify
first component selected from physiological carriers and immunostimulants, and a second component selected from the above	TAX	cancer ai
polypeptide, polynucleotide, antibody, fusion protein, T-cell population and antiden-presenting cells that express the above polypeptide.	Sd	Claim 1;
stimulating an immune response in a patient (comprising administering to the matient the above commonstion) traction duron cancer in a matient	88	The inver of 120 10
comprising administering to the patient the above composition and a diamonetic vit (commistering to the patient the above composition and a	85	specifica diven in
at least one antibody cited above and a detection reagent, where the	388	invention
detection reagent comprises a reporter group). The composition and methods are useful in diagnosing, preventing and treating cancer,	888	They are
particularly lung cancer. The present sequence is a lung cancer- associated antigen cDNA of the invention.	386	invention of ending
Sequence 295 BP; 52 A; 88 C; 88 G; 67 T; 0 U; 0 Other;	38 	encodes a

T; 0 U; 0 Other; 67 ö 88 ΰ 88 Α; 52 BP; 295 Sequence

1782 1842 1902 1962 ö 180 240 120 60 ention describes an isolated human nucleic acid (I) encoding any 10-1533 residue amino acid sequences (S1), given in the action, comprising any of 164 179-11421 base pair sequences (S2), on the specification. The methods and compositions of the present on are useful for identifying, diagnosing, monitoring, staging, and trating lung cancer and non-cancerous diseases of the lung. and used for identifying lung tissue, monitoring and ying and/or designing antagonists of the polypeptide of the nor, gene therapy, production of transgenic animals and production a lung tissue for treatment and research. This sequence a lung specific nucleic acid tted human nucleic acid molecule and polypeptide, useful for ing, diagnosing, monitoring, staging, imaging and treating lung ad non-cancerous diseases of the lung. sne therapy; vaccine; lung specific antigen; cancer diagnosis; onitoring; cancer staging; cancer imaging; lung cancer; erous diseases of the lung; transgenic animal; gene; ss. AGGATGGACGCCTCAAAATGGAAGGAGTCCCCACGGGAGGATGGGTCCGAGGTCCGGCTGTG CTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGGGGGG CTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCGCCTCAGCTTGGTGGTGGTTTTGAGGG GCCGCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGG GCCCCCCCCCCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCGCCTTGG AGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTG GCCATCCAGCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGG Gaps .: 0 295; 0; Indels Length Score 295; DB 10; Pred. No. 4.7e-70; 0; Mismatches 0; ΰ Liu Sun Y, sific nucleic acid (LSNA) #90. Page 238; 389pp; English. 10.7%; Scc. 100.0%; Pre ς, Ω ЦЦ Chen standard; cDNA; 251 001; 2001WO-US043612. 000; 2000US-0252500P. 003 (first entry) Conservative A, Recipon H, JIADEXUS INC 2-713376/77. imilarity 533-A2. ens. 02. ....

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pluripotent cells. The pluripotent cells and partially or terminall differentiated cells can be used in allo-, concomitant- or xeno-transplantetion, cell therapy, tissue and organ augmentation or replacement, and gene therapy. They can also be used for producing chimeric or transgenic animals

- Sequence 736 BP; 202 A; 147 C; 174 G; 213 T; 0 U; 0 Other;

atch2.8%;Score 76.6;DB 3;Length 736;191;Conservative0;Mismatches59;10;2411Cruterceagartegereacrerrangeres59;10;112411	
DB 3; Length 736; e-10; 59; Indels 29; Gaps regreedsratrorsceedsrat 1011, 011, 11, 11, 12, 12, 12, 12, 12, 12, 12,	
DB 3, Length 736; e-10; 59; Indels 29; rggreggagratcraftagg                                   	
DB 3; Length 7 e-10; 59; Indels TGGTGGGAGTATCTG TGGTGGGAGTATCTG                     	
DB 3, Le 6-10; 59; 1 10, 10, 10 10, 11, 10, 10 10, 11, 10, 10, 10, 10, 10, 10, 10, 10,	
Score 76.6; DB 3; Pred. No. 5.4e-10; 0, Mismatches 59; CTCTTTCTAAGGTGGTG CTCTTTCTAAGGTGGTGG TGTCTTTCTAAGGTGGTGG TGTCTTTTTTTTTAAGGTGCTGGG TGTCTTTTTTTTTAAGGTGCTGGGG TGTCTTTTTTTTTACCTGAATAA [	
Scort Pred MCTCTT MCTCTT MCTCTT MCTCTT MCTCTTT MCTCTTT MCTCTTT MCTCTTT MCTCTTTTT MCTCTTTTTTTT	38 BP.
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- AAK90877;
- 05-NOV-2001 (first entry)
- Human digestive system antigen genomic sequence SEQ ID NO: 4453.

- Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ds.
- Homo sapiens.
- WO200155314-A2.
- 02-AUG-2001.
- 17-JAN-2001; 2001WO-US001324

- 31-JAN-2000; 2000US-0179065F 24-FEB-2000; 2000US-018628F 24-FEB-2000; 2000US-0186654F 02-MAR-2000; 2000US-01805474F 17-MAR-2000; 2000US-01807474 17-MAR-2000; 2000US-019076F 19-MAY-2000; 2000US-0190176F 19-MAY-2000; 2000US-02034657F 07-JUN-2000; 2000US-0215135F 07-JUN-2000; 2000US-0216477F 28-JUN-2000; 2000US-0216477F 07-JUL-2000; 2000US-0216477F 07-JUL-2000; 2000US-0216477F 07-JUL-2000; 2000US-0216477F 2000US-0216880P. 2000US-0217487P. 2000US-0217496P. 11-JUL-2000;

14-JUL-2000; 2000US-0218290P. 26-JUL-2000; 2000US-0220963P. 26-JUL-2000; 2000US-0220963P.

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AAS30028/c ID AAS30028 standard; DNA; 32038 BP. XX AC AAS30028; DT 21-NOV-2001 (first entry) XX DT 21-NOV-2001 (first entry) XX DE Human lung antigen genomic DNA #98.	XX Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog; KW chicken; sheep; immunosupressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; KW ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; Myperproliferative disorder; breast; liver; cardiovascular disorder; ds; KW fungal infection; viru infection; system disorder; endocrine disorder; KW dungal infection; viru disorder; respiratory disorder; KW wound healing; skin aging; organ transplantation; food preservative; KW wound saptens. XX WO200155303-A2.	02-AUG-2001. 17-JAN-2001;	51-UAN-2000 04-FEB-2000 24-FEB-2000 02-MAR-2000;	16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 19-MAY-2000; 07-JUN-2000;	28-JUN-2000; 30-JUN-2000; 07-JUN-2000;	FR 07-UUL-2000; 2000US-021680F. FR 11-UUL-2000; 2000US-0217487P. FR 11-UUL-2000; 2000US-0217487P. FR 14-UUL-2000; 2000US-0218290F. FR 14-UUL-2000; 2000US-0218290F. FR 14-AUG-2000; 2000US-0224518P. FR 14-AUG-2000; 2000US-0224518P. FR 14-AUG-2000; 2000US-0224513P.	14 - AUG - 2000 14 - AUG - 2000 14 - AUG - 2000 14 - AUG - 2000	14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;	14 - AUG-2000 18 - AUG-2000 22 - AUG-2000 22 - AUG-2000 22 - AUG-2000 30 - AUG-2000 30 - AUG-2000	01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000
17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000	ССССССССССССССССССССССССССССССССССССС	08-DEC-2000; 11-DEC-2000; 05-JAN-2001;	Rosen CA,	DR WPI; 2001-502630/55. XX PT Polynucleotides encoding digestive system antigens, useful for PT diagnosing, treating, preventing and/or prognozing disorders of the PT digestive system, particularly cancer and cancer metastases.	Disclosure; SEQ ID NO 3556; 986pp;	The present invention provides the protein and coding sequences of a commoler of human digestive system antigens. These can be used in the CC number of human digestive system antigens. These can be used in the CC diagnosis, treatment and prevention of digestive system disorders, CC including cancer, Meckel's diverticulum, bacterial or parasitic transformers, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative system antigen of the invention NA fragment XX Semence 32018 BP 9776 A 54547 (5463 d: 10823 T. O. D. D. D. D. D. D. S. Semence 32018 BP 9776 A 5454 d: 10823 T. O. D. D. D. D. D. D. D. D. S. Semence 32018 BP 9776 A 5454 d: 10823 T. O. D. D. D. D. D. D. S. S. Semence 32018 BP 9776 A 5454 d: 10823 T. D. S. S. Semence 32018 BP 9776 A 5454 d: 10823 T. D. S. S. Semence 32018 BP 9776 A 5454 d: 10823 T. D.	occurred of the second se	QY 1013 AAAAAAAATTUTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATT 1072 	QY     1073     GTATTTTGGATTTATCAATTTAAAAATTGTGGAAATTTGTTTG	Db       28759 GTATCTACATACAATCTCACATTTACCTCTTAGCCCACAAAGCTTATTACTAT       28700         Qy       1179 CTAGCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGAACC       121         Db       28699 CTGGCCCTTATAGAAAAGTTTCCTGACCTCGAGCC       1221         Db       28699 CTGGCCCTTATAGAAAAAGTTTCCTGACCTCGAGCCTAGAGC       28657         RESULT 13       3

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		also	r	a Bo	਼ ਜ਼ਰੇ ਜ਼	5	1072 <sup>°</sup> 28818	1125 28760	1178 28700
		enting and/ or prognosing ng including lung cancers and s.	1.	Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode the lung antigen polypeptides of the invention. Lung antigen polypeptides treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A mice, rabbits disorders include autoinmune disorders in e.g. humans, hyperproliferative disorders such as rheumetoid arthritis, hyperproliferative disorders such as neumatoid arthritis, disorders such as cerdiac arrest, creebrovascular disorders such as cardiac arrest, creebrovascular disorders such as cerdiac arrest, viruses and fungi, ocular disorders such as corneal infection, endocrers such as premature absorders such as corneal infections caused by bacteria, viruses and fungi, premature labour and infectility, gastrointestinal disorders such as crown reading as corneal infections endocrers such as from the such as corneal infections endored are been and fungi, premature labour and infectility, gastrointestinal disorders such as crown's disease, renal disorders such as glomerulonephricie and	ma and pleurisy. The polypeptides can to prevent skin aging due to sunburn intation, to regenerate tissues and in 1so be used as a food additive or se storage capabilities. Note: The not form part of the printed electronic format directly from WIPO sequences	; DB 5; Length 32038; : 1.3e-08; :ches 60; Indels 16; Gaps	aaaaaaaaateertattittagragacatgtatttaccaaaaafatgtacfcaaftatt 1 	TATTAA	caacataatattgattttgcctcttggcrctgaagcccaaatatttaccgt 1 
200005-02492657 200005-02492657 200005-02492697 200005-02493007 200005-02501607 200005-02501607 200005-02519807 200005-02519807 200005-02519807 200005-02518667 200005-02518667 200005-02518697 200005-02518697 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897 200005-02519897	AN GENOME SCI INC. Barash SC, Ruben SM;	e for treating rs related to ection e.g. di	SEQ ID NO 292; 507pp; English	0164 ptides orses for of orses be rdent be rdent for tite fertification fertification	respiratory disorders such as asthma and pleur also be used to aid wound healing, to prevent to maintain organs before transplantation, to chemotaxis. The polypeptides can also be used preservative to increase or decrease storage c sequence data for this patent did not form par specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences	2.7%; Score 75; DB larity 65.9%; Pred. No. 1.3 Conservative 0; Mismatches	AAAAATTCTTATTTTAGTAGACA 	GTATTTTGGATTTTATCATTTAAAAATTGTGGGAAATTTGTTTG	caacataatattgattttgcct                           ctacataacaatctcagttttacct
17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 01-DEC-2000 01-DEC-2000 05-DEC-2000 05-DEC-2000 06-DEC-2000 06-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000	(HUMA-) HUMAN Rosen CA, Ba:	WPI; 2001-457723/49 Isolated polypeptid respiratory disorde for testing and det	Claim 1; SEQ	Sequences AAS29931-AAS3 the lung antigen polype and their associated po treatment and prevention mice, rabbits, goats, h pathological condition absence of a mutation hyperproliferative diso hyperproliferative diso hyperproliferative diso hyperproliferative diso cardiovascular disorders disorders such a ocular disorders such a prematue labour and i Crohn's Aisease, in	respiratory dis also be used to to main orco chemotaxis. The preservative to sequence data i specification, at ftp.wipo.int	Query Match Best Local Simil Matches 147; C	1013 AAA/     28877 AAA	1073 GTA     28817 G1	1126 28759 GTA
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cm gene therapy; lung antigen; neoplasia; acute myelogenous leukaemia; m adenocarcinoma; respiratory disorder; chronic rhinitis; sinusitis; immunodeficiency; X-linked agammglobulinaemia; m x-linked infantile agammglobulinaemia; m x-linked infantile agammglobulinaemia; m von willebrand's disease; bleeding disorder; thrombocytopenia; w willebrand's disease; acquired platelet dysfunction; kidney failure; multiphe myeloma; macrophage related disorder; daucher's disease; w willibbrand's disease; acquired platelet dysfunction; kidney failure; multiphe myeloma; macrophage related disorder; daucher's disease; w multiphe myeloma; macrophage related disorder; falorer disease; w renal disorder; heeker's muscular dystrophy; bowleg; musclar dystrophy; nervous disorder; ischaemic lesion; conticosterion; endorrine disorder; Cushing's syndrome; conticosteroid deficiency; gastrointestinal disorder; dysphagia; gastric reflux; human; ds. 28699 CTGGCCCTTTATAGAAAAAGTTTCCTGACCTCTGCCCTAGAGC 28657 Human novel lung related polypeptide DNA SEQ ID NO 292. RESULT 14 ADB33365/c ID ADB33365 standard; DNA; 32038 BP. 31-JAN-2000; 2000US-0179065P 24-FEB-2000; 2000US-0180628P 24-FEB-2000; 2000US-0180628P 02-MAR-2000; 2000US-0180874P 17-MAR-2000; 2000US-0199076P 19-MAY-2000; 2000US-0190076P 19-MAY-2000; 2000US-0190076P 20-JUN-2000; 2000US-02148667 11-JUL-2000; 2000US-02166477 07-JUL-2000; 2000US-02166477 11-JUL-2000; 2000US-02166477 11-JUL-2000; 2000US-02166477 11-JUL-2000; 2000US-02174966 11-JUL-2000; 2000US-02174967 11-JUL-2000; 2000US-0218647 11 2000US-0225447P 000US-0225757P. 000US-0225758P. 00US-0225759P 000US-0226681P 22-FEB-2002; 2002US-00079854 000US-0226279P 00US-0226868P 2000US-0227182P 2000US-0227009P (first entry) US2003054368-A1. 14-AUG-2000; 2 14-AUG-2000; 2 14-AUG-2000; 2 22-AUG-2000; 23-AUG-2000; Homo sapiens. 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 18-AUG-2000; 22-AUG-2000; 22-AUG-2000; 04-DEC-2003 20-MAR-2003 ADB33365; g 

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QY     1126    CAACHTATATATGATTTTGCCTCTGAGGCCTGAAAGGCCTAAATATTTACGGT     11       Dh     28759     GTATCTAACAATAACAATCGGTTTTAGCCCTTTAGCCCAAAGGCCTAAAATATTTACTAT     28700	1110 0 0011110001000000000000000000000	Db 28699 CTGGCCCTTTATAGAAAAAGTTTCCTGACCTCTGCCCTAGAGC 28657		RESULT 15 ADJ12644	ID ADJ12644 standard; DNA; 32844 BP.	AX AC ADJ12644;	XX DT 20-MAY-2004 (first entry)		DE DNA fragment of a BAC clone that encodes a numan secreted protein sey. XX	XW human; secreted; cancer; haematopoietic disease; anaemia;	XW multiple ageneration reproductive group disease; systemic lupus erythematosus XW inguinal hernia; musculoskeletal disease; systemic lupus erythematosus	KW gout; cardiovascular disease; arrnythmia; hypernatraemia; retai diseas KW fetal alcohol syndrome; Down's syndrome; excretory disease;	KW urinary incontinence, renal disorder; neural; sensory disease; xw alzheimer's disease; meninoitis; respiratory disease; emphysema;	XW occupational lung disease; endocrine disease; diabetes; w occupational lung disease; endocrine disease; portal humertension;	KW irritable bowel syndrome; epithelial disease; scleroderma;	<pre>KW epidermolysis bullosa; cytostatic; antianemic; antiarthitc; KW antiasthmatic; anti-HV; immunosuptresive; antiinflammatory; </pre>	<pre>KW antipsoriatic; antibacteriat; osteopaulic; defmactoryteat; antiscue; KW immunomodulator; antiarrhythmic; cardiant; notropic; antilipemic; KW immunomodulator; antiarrhythmic; cardiant; notropic; antilipemic;</pre>	KW nephrotropic; uropathic; neuroprotective; antipatkinisonian; uranyuitte KW antidiabetic; anabolic; hypertensive; vulnerary; ds.	XX OS Homo sapiens.	AA US2004010132-A1.	AA PD 15-JAN-2004.	AA PF 30-OCT-2001; 2001US-00984429.	09-0CT-1997;	09-0CT-1997	09-0CT-1997	PR 09-0CT-1997; 97US-0071498P. PR 08-0CT-1998; 98W0-15021142.	01-NOV-2000	(ROSE/)	(DUAN/) (PURN/)	(FLOR/	(/NUOY)	(YUGG/) (YUGG/)	(OLSE/) EBNER R. (OLSE/) OLSEN H.	XX PI Rosen CA, Brewer LA, Duan RD, Ruben SM, Florence KA, Greene JM; of Vound DF Ferrie AM YurG, Florence C, Ebner R, Olsen H;	WPT: 2004-090518/09.
17-NOV-2000; 2000US-0249211P. 17-NOV-2000; 2000US-0249212P. 17-NOV-20000: 20249212P.	17-NOV-2000; 2000US-024921.4P. 17-NOV-2000; 2000US-0249214P.	17-NOV-200U; 200US-0249215F. 17-NOV-2000; 2000US-0249217F. 17-NOV-2000; 2000US-0249217P.	17-NOV-2000; 2000US-0249218P. 17-NOV-2000: 2000US-0249244P	17-NOV-2000; 200005-0242411. 17-NOV-2000; 2000US-024245P.	I7-NOV-2000; 200005-0249265F.	17-NOV-2000; 2000US-0249297P. 17-NOV-2000; 2000US-0249299P.	17-NOV-2000; 2000US-0249300P. 01-DEM-2000; 2000US-0250150P.	01-DEC-2000; 2000US-0250391P.	05-DEC-2000; 2000US-0251030P. 05-DEC-2000; 2000US-0251988P	05-DEC-2000; 2000US-026719P.	06-DEC-2000; 2000US-U251479P. 08-DEC-2000; 2000US-0251856P.	08-DEC-2000; 2000US-0251868P. 08-DEC-2000; 2000US-0251869P.	08-DEC-2000; 2000US-0251989P.	1-DEC-2000;	05-JAN-2001; 2001US-0259678P. 17-JAN-2001; 2001US-00764878.	(HUMA-) HUMAN GENOME SCI INC.	Rosen CA, Ruben SM, Barash SC;	WPI; 2003-695900/66.		diagnosing acute myelogenous leukemias, adenocarcinoma, turombocycopenia, Von Willebrand's disease.	Disclosure; SEQ ID NO 292; 178pp; English.	The invention relates to an isolated lung antigen polypeptide sequence or	encoded sequence in a CDNA clone. The polypeptide and its polynucleotide are useful for treating, preventing, diagnosing and/or prognosing	diseases and/or disorders such as parhological cell proliferative neoplasias e.g. acute myelogenous leukaemias, adencarcinoma; respiratory	disorders such as chronic rhinitis, sinusitis; immunodeficiencies such as X-linked aqammaqlobulinaemia, X-linked infantile agammaglobulinaemia;	inflammatory disorders such as adrenalitis, alveolitis; immune complex diseases such as serum sickness, polyarteritis nodosa; bleeding disorders	such as thrombocytopenia, Von Willebrand's disease; acquired platelet dysfunction such as kidney failure, multiple myeloma; disorders	associated with macrophage numbers and/or macrophage function such as Gaucher's disease, Neimann-Pick disease; tumours such as colon cancer,	pancreatic cancer; renal disorders such as kinney fallure, nephritis; bone disorders such as Albers-Schonberg disease, bowlegs muscile disorders products and disorders, bowlegs musciles	disorders such as becker's muscular dystrophy, buchenne s muscular dystrophy, nervous disorders such as ischaemic lesions disorders and a solvention of the second of the second second second second second second second second second	) endocrime disorders such as cusming's syndrome, culticosteroid	Jery Match 2.7%; Score 75; DB 10; Length 32038; Sagt Local Similarity 65.9%; Pred. No. 1.3e-08; 1.3e-08; 1.4; Gang 2; Protec 147: Concervative O: Micartohec 60; Indels 16; Gang 2;	ATTCTTATTTTTAGTAGAGATGTATTTACCAAAAATATGTACTGATTATT 10	28877 AAATATTTTAATTAATTAATTAATTAAACCCCGTATTACAAAAAAATTCFTCTAAATTATT 28818	1073 GTATTTTGGATTTTATCAATTTATAAAAATTGTGGGAAATTTGGTCTTACGC 1125

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treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's disease.

Disclosure; SEQ ID NO 498; 286pp; English

This invention relates to novel polynucleotides encoding human secreted proteins. Specifically, it refers to the vectors, host cells, recombinant and synthetic methods for producing human polynucleotides, polypeptides and synthetic methods for producing human polynucleotides, polypeptides and antibodies. Furthermore, it relates to screening methods to identify agonists and antagonists that can be used to inhibit or enhance the production and function of the secreted proteins. The present invention describes these compositions as useful for disgnosing, treating or preventing disorders such as cancer, haematopoletic diseases including preventing disorders such as cancer, haematopoletic diseases including prostatitis and hypernatraemia, mixed fetal diseases including prostatitis and hypernatraemia, mixed fetal diseases including systemic lupus erythematosus and gout, cardiovascular diseases including teal producing emphysema and occupational lung diseases including teal hypernatraemia, mixed fetal diseases including continary incontinence and renal disorders, neural or sensory disease including diabetes and glomerulonephritis, respiratory diseases including diabetes and glomerulonephritis, digestive diseases including portal hypernation and irritable bowe and condering diseases including diabetes and glomerulonephritis, digestive diseases including cort, there are various activites such as cytostatic, antianthrit, antibatory, antipout, immunosuppressive, antistritic, antisthmatic, antibator, antiarthythmic, cardiant, entitratritic, antistontatic, antibator, antiarthythmic, cardiant, move secreted protein of the invention. Weretensive antiparkinsonian, tranquilizer, antibator, antiarthythmic, cardiant, antiparkinsonian, tranquilizer, antibator, antiarthythmic, cardiant, antiparkinsonian, tranquilizer, antibator, antiarthythmic, cardiant, move secreted protein of the invention. Weretensive desense including secreted protein of a bollowing we site www.secdata.uspto.gov/sequence.html, pocument 10; soluonin132. Sequence 32844 BP; 11125 A; 6089 C; 5587 G; 10043 T; 0 U; 0 Other; 

2 1126 -----CAACATAATATTTGATTTTGCCTCTTGGCTCTGAAAGCCCCAAAATATTTACCGT 1178 4086 GTATCTACATAACAATCTCAGTTTTACCTCTTAGCCCACAAAGCCTAAAATATTTACTAT 4145 1013 AAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATT 1072 1073 GTATTTTGGATTTTATCAATTTAAAAATTGTGGAAAATTTGCTCTTACGC------ 1125 60; Indels 16; Gaps 2.7%; Score 75; DB 12; Length 32844; 55.9%; Pred. No. 1.3e-08; ive 0; Mismatches 60; Indels 16; 1179 CTAGCCCGTTACAGAAAAGTCTGCTGACTACTGAGCCAGACC 1221 65.9%; Local Similarity 65.9 nes 147; Conservative Query Match Best Loca Matches q  $\delta$ q qq  $\mathcal{S}$ 8 8

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GenCore version 5.1. Copyright (c) 1993 - 2004 Comp	eic – nucleic search, using sw model November 29, 2004, 08:42:07 ; S	(wit 1124	US-09-989-920-100 : score: 2754 : 1 gccagaagcagcctcagctt	g table: IDENTITY NUC Gapop 10.0, Gapext 1.0	ed: 4526729 segs, 23644849745 residues	number of hits satisfying chosen parameters	a DB seq length: 0 a DB seq length: 200000000	processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	0 	Pred. No. is the number of results predicted score greater than or equal to the score of t and is derived by analysis of the total score	& Quer Matcl	27754       100.0       2754       6       AX555073         2718       98.7       211305       9       AC079988         2397.4       98.7       225203       5       AC140107         2397.4       98.7       225203       5       AC140107         2397.4       98.7       225203       5       AC140107         2397.4       98.7       225203       5       AC130359         820.6       5       AR204690       80365       AC1303359         820.6       5       AR204690       63.5       AC1303359         612.4       88036       2       AC1303359       612.4         612.4       9       20.1       611       G38425         355.4       9.06       6       AX535076       6         357.4       9.1       0.1       G38425       6         357.4       9.1       0.1       G38425       6       6       AX535076         87.6       9.1       0.1       G38425       6       AX535076       6       6       6       6       7       6       2       6       6       7       2       2       2       2       2       2
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<ol> <li>CCCCAAAAGCAGGGTTGGATTGCTTCTURAGCCGGGTTCGAACATGGAGTTGCAAAGGAGGTTGCAAAGGAGGTTGGAATGCTTCGAGTGGGATTGCTTCGGATGCAAGGAGTTGCAAGGAGTTGCAAGGAGTTGCAAGGAGTTGCAAGGAGTTGCAAGGAGTTGCAAGGAGTTGCAAGGAGTTGCAAGGAGTTGCAAGGAGTTCCAAGGAGGAAGGA</li></ol>	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chamistry, or coverd by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.	MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc	SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and cowrkers at http://www.chori.org	NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP11-60M20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-795C1; actual end is at base position 111002 of RP11-6906.	Single plasmid region exists between 76851 and 76869. Polymorphisms exists between AC067960, AC013399 and AC079988. Data from AC067960 and AC013399 was used to finish AC079988. Data from AC067960 FEATURES Location/Qualifiers source 1. 211308 /organism="Homo sapiens" /mol_type="genomic DNA"	<pre>/ullianset = caronisode /map="2" /clone="kP11-795C1" /clone="kPC1-11" repeat_region 1115 repeat_region 1042.1153 /rpt_family="MER1_type" repeat_region 1682.1153</pre>		repeat_region 2371raminy= Aid repeat_region 2371s183 repeat_region 2491s183 repeat_region 3648s1369 repeat_region 7505_family="MIR"	repeat_region 3726333 repeat_region 4744149"MIR" repeat_region 43754466 repeat_region 42754466 repeat_region 46274725 repeat_region 48254920
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Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGeraid,M., Gage,D., Galagan,J., Cardyna,S., Graham,L., Grand-Pierre,N., Hulme,M., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,M., Jliev,L., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,R., Macdonald,P., Major,J., Maningy.J., Matthews,C., McCarthy,M., Meldtim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., OC Connor,T., O'Donnell,P., O'Nell,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Spencer,B., Stange-Thomann,N., Stojlanovic,N., Stubs,M., Vassiliev,H., Venkataman,V.S., Viel,R., Voham, H., Mu,X., Wiman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M., Direct, Submission Submitted (21-FEB-2003) Whitehead Institute/MIT Center for Genome Submitted (21-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasKer: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html ------ Genome Center Center: Whitehead Institute/ MIT Center for Genome Research arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is Conserves quality: 224530 bases at least 020 Insert size: 221000; agarose-fp Insert size: 224903; sum-of-contigs Quality coverage: 14.9 in Q20 bases; sum-of-contigs Quality coverage: 14.6 in Q20 bases; sum-of-contigs 46920: contig of 46920 bp in length 47020: gap of 100 bp 51090: contig of 4070 bp in length 51190: gap of 100 bp 163725: contig of 112535 bp in length 163825: gap of 100 bp 163825: contig of 61378 bp in length. ដ្ /clone="RP11-1201C10" /clone\_lib="RPCI-11 Male BAC segment 47021. 51090 /note="assembly\_fragment" note="assembly\_fragment" .225203
 /organism="Homo sapiens" /mol\_type="genomic\_DNA" /db\_xref="taxon:9606" /chromosome="17" Location/Qualifiers clone\_end:SP6\_\_\_\_\_\_vector\_side:left" 51191. .163725 Center code: WIBR .225203 'map="17" 47021 51091 51191 163726 163826 46921 misc\_feature misc\_feature misc\_feature source JOURNAL FEATURES TITLE ""COMMENT

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2456 ATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGTGGGGGAGTAT 2515

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299       ATGTAACCTCACACCTTCTC10111111         219       ATGTAACCTCACACCTTCTCCAAATTG         516       CTGTCGGGGTGGTGTGGCCTTTCTCCAAATTG         239       CTGTCGGGGTGGTGTG11111111111111111111111	<pre>NK Sequence 3 from patent US 6368794. AR204690 1 G1:21502081 AR204690.1 G1:21502081 Unknown. Unknown. Unclass1 to 1853) 1 (bases 1 to 1853) 3 Daniel,S. Gilmore,J., Stuart,S.G. and Stuve,L.L. Detection of altered expression of genes regulating cell proliferation proliferation Proliferation Patent: US 6368794-A 3 09-APR-2002; Detection of altered expression of genes regulating cell proliferation Proliferation Proliferation Patent: US 6368794-A 3 09-APR-2002; Detection of altered expression of genes regulating cell proliferation Patent: US 6368794-A 3 09-APR-2002; Cce 1.01853 Anton proliferation Mol_type="unassigned DNA" (atch 63.53; Score 1747.6; DB 6; Length 1853; fatch 63.53; Pred. No. 0; S 1750; Conservative 0; Mismatches 4; Indels 0; Gs</pre>	0y994TGTTTTCCCCCCATCACAAAAAAAAATTCTTATTTTTATAGTAGACATGTATTTACCAA1053111671711111111111111111111111111111111111

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	29.8%; Score 820.6; DB 2; Length 88036; imilarity 77.9%; Pred. No. 7.7e-193; ; Conservative 0; Mismatches 238; Indels 0; Gaps 0;	rccreasaacccccacrragcrrccagaccrrrcrgcaaaagcrccrccregcrrrccrcc 486	 THNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	CTCCCCCAATCTATGGGTCACAGGTTAACAGGATCTGAGGGGCAAGTGGCTAGTGGGCCA 546	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	GGGCTGCCACCCTGGCCACTTTAGGGCCTTCTAGGGCAGTGTCCTTA         606	36AAGTAGCTCTGAGGCATGGGTTTTCTGCTGCTGCTGGGGCAGCTGATGGGATAAGGT 666		GGGGAAGGACGGTCAGTGCTTGGGCCCAGCCTGGCCAGCCTGGCGATGGGGAAACCAAAC 726	GEGGAAGGACGETCAGTCCTTGGGCCCCGGCCTGGCCTGG	CATGFCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTGAGGAG 786 	CCCTGAGGTGGGCAGCAGGGGCAGGGGAAGTTTTCAGGCCTTCATCAAGAGAACAACA 846	CCTGAGTGGCAGCAGGGGCCAGGGGGAAGTTTTCAGGCCTTCATCAAGAGAAGAACAACA 72708	TCCTCAGCTCCGACCCCTCATCCTGTATCAGGACTTACCGGTGTGTGGACTGCCCTTGTC 906	AGCTAGGATACGGTGGGCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAG 966	AGCTAGCATACGGTGGGCCCACCGGGCCCACTGGCTGTTTATGCCACTGATTTATGATAG 72588	GGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAA	TATTTTAGTAGTATTTCCAAAAATATGTACTCAATTATTGTATTTTGGATTTT         1086	TATTTTAGTAGACATGTATTTTCCAAAAAATATGTACTCAATTATTATTTTTGGATTTT 72468	arcaartraaaaarrgreeaarrrertrecrertaceccaacaraararreger 1146	72	TCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAGTCTGCTGA 1206	тсттеестстевалассссалалтаттассетствесссеттасабалалатстестея 72348	CTACTGAGCCAGACCTCCATCCCCCTGTTGGATTATTTAAGAAAGCCTCAGA 1266	7	CAGTAAGGGCTTTTTTTAAAAGGATAAAATGACTTGGTTGG	CAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGGGCTTGGAAGGAGGGGAAGG 72228	AGATGAGGGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGGGTGGC 1386	ATTCAGATGAGGGTTTCTGAATTCCANCCCCAGGGGGGGGGG	TGGCGAGCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTG
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pb     72167     NINNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	RESULT 7 AC139359 AC139359 AC139359 AC139359 AC139359 AC139359 LOCUS B0036 bp DNA LOCUS AC139359 AC139359 AC139359 AC139359 ACCESSION AC139359 ACCESSION AC139359 ACCESSION AC139355 ACCESSION ACCESION ACCESION ACCESION ACCESION ACCESION ACCESION ACCESION AC	<pre>Birren.B., Vusbaum,C. and Lande Birren.B., Nusbaum,C. and Lande Homo sapiens chromosome 17, clc Unpublished 2 (bases 1 to 88036) Birren.B., Nusbaum,C., Lander,E Anderson,S., Arachchi,H.M., Bar Boguslavkiy,L., Boukhgalter,B., Boguslavkiy,L., Boukhgalter,B., Collymore,A., Cook,A., Cooke,P. Collymore,A., Cook,A., Cooke,P. Diaz,J.S., Dodes,S., booley,K., Gag Graham,L., Grand-Pierre,N., Hall, Hall,J., Horton,L., Hulme,W., I Kamat,A., Karatas,A., Kells,C., Kamat,A., Karatas,A., Kells,C., Lindblad,A., Karatas,A., Kells,C., Lindblad,A., Karatas,A., Lui,A., Lui,A., Lindblad, C., Lui,A., Lui,S., Lui,A., Lindblad, Lui,A., Lui,S., Lui,A., Lui,A., Lindblad, Lui,A., Lui,S., Lui,A., Lindblad, Lui,A., Lui,S., Lui,A., Lindblad, Lui,A., Lui,S., Lui,S., Lui,A., Lindblad, Lui,A., Lui,A., Lui,A., Lui,A., Lindblad, Lui,A., Karatas,A., Karatas,A., Lui,A., /pre>	<pre>Macdonald,P., Major,J., Manning,J., Mati Weldrim,J., Meneus,L., Mihova, T., Mleng Nguyen,C., Nicol,R., Norbu,C., O'Connor, O'Neil,D., Ollver,J., Peterson,K., Phuni Rachupka,A., Ramasamy,U., Raymond,C., Re Roman,J., Schauer,S., Schupback,R., Sear Spencer,B., Stange-Thomann,N., Stojanovi Talamas,J., Tesfaye,S., Theodore,J., Toy Vassillev,H., Venkataraman,V.S., Viel,R Wyman,D., Yonng,G., Zainoun,J., Zembek,I DURNAL Submitsion Instit JOURNAL Submitted (01-FEB-2003) Whitehead Instit</pre>	0 0 1 2 4 6 5	<ul> <li>NOTE: This record contains 94 individual</li> <li>sequencing reads that have not been assembled into</li> <li>contigs. Runs of M are used to separate the reads</li> <li>and the order in which they appear is completely</li> <li>arbitrary. Low-pass sequence sampling is useful for</li> <li>identifying clones that may be gene-rich and allows</li> <li>coverlap relationships among clones to be deduced.</li> <li>However, it should not be assumed that this clone</li> <li>will be sequenced to completion. In the event that</li> <li>the record is updated, the accession number will</li> <li>be preserved.</li> <li>856: contig of 856 bp in length</li> </ul>

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QY       921       GGGCCCACCTGGCCCACTGGCTTATGCCACTGATTATGATAGGGAATATTATCTTT       980         Db       82618       GGGCCCACCGGGCCCACTGGCTGTTATGCATAGGGAATATTATCTTT       980         QY       981       [	Qy       1101       TGTGGAAATTTGTTTGCTCTTAGGCCAACATAATTTGATTTGGCTCTGAAA       1160         Db       82798       [	Qy         1281         Tranangarpanangartnggertnggertnggargeggargegargegargegg         1340           Db         82978         [	Db       B3158       GAIdaGCUTTIGCTTUTIGCTUTTIGCGCCCCTGGTTCTTGGGGACCGCGGGGCC       B3217         Qy       1521       TTTGGTCTGCATCCCCTGGCGCGGGGGTGGGGGGGGGGG	RESULT 6 AX535072 AX535072 960 bp DNA linear PAT 22-NOV-2002 LOCUS Sequence 99 from Patent W002068633. ACCESSION AX535072.1 G1:25261751 ACCESSION AX535072.1 G1:25261751 ACCENTIME Compositions (human) ACCESSION AX535072.1 G1:25261751 ACCESSION AX53751751 ACCESSION AX53751751 ACCESSION AX53751751 ACCESSION AX53751751 ACCESSION AX53751751 ACCESSION AX53751751 ACCESSION AX53751751 ACCESSION AX551751 ACCESSION AX551751 ACC
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1717 1777 1837 1897 2017 2077 2196 ŝ 1957 2137 CCAGTCCGGAT-CCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGGACAAGTTCTTTTG 2255 280 340 400 460 520 580 PAT 30-JAN-2004 160 220 640 41 GTACCTTGGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAGCCTCCTTCCCATGTG 100 Homo sariens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Schlegel,R., Endege,W.O. and Monahan,J.E. Genes differentially expressed in human prostate cancer and their 1778 GAGGGGCCGCCCCGGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC 281 CTGTGGCCATCCAGCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCTGGTGTGTCTTCACT CCAGGGGCAGACCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTAGTAGCAG 521 GATGGGGGCCAGGGTCCCACATGCTGCTGATGCCCGAGCCAGGTTGAGCTTCCTGGTGT 581 CCAGTCCGGATCCCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTG GTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAGGCTCTTCCCATGTG TCCA6CT6CTCTTCCT6CTACAAAGGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTT rccagcrgcrtcrtccrgcrazaaggggacrgcrcacagrggccrcagcrtggrgrrrr 161 GAGGGGCCCCCCCGGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTCCCATCTGCC 1838 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGGGTCCGG 221 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGGG CTGTGGCCATCCAGCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACT CCAGGGGCAGCAGCAGCAGCTGCAGTTCCTTCCTTCGTGAGTAACAGTAGTGATAGCAG CCCTAAAGCAATGGGGGGGGCCCCCCCTAGCCCCAGTTTCCAGGAAGTCAACTGGGAGGTTA 461 CCCTAAAGCAATGGGGAGGCCCCCACTAGCCCCAGTTTTCAGGAAGTCAACTGGGGAGGTTA 2138 GATGGGGGCCAGGGTCCCACA-GCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGT Gaps TCACAGTGCTGG - CTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGCTC 2304 ŝ Score 612.4; DB 6; Length 960; Pred. No. 4e-141; 0; Mismatches 1; Indels 3 linear Patent: W0 0160860-A 54549 23-AUG-2001; Millennium Predictive Medicine, Inc. (US) Location/Qualifiers DNA CQ522682 611 bp DN Sequence 54549 from Patent WO0160860. CQ522682 /mol\_type="unassigned DNA" /db\_xref="taxon:9606" /organism="Homo sapiens" CQ522682.1 GI:41488946 Query Match 22.2%; Best Local Similarity 99.4%; Matches 646; Conservative C Homo sapiens (human) 5 use 1658 1718 101 1958 341 2078 1898 641 2197 2256 RESULT 9 CO522682 LOCUS source ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE MUTHORS JOURNAL ", FEATURES TITLE ORIGIN ିର ଶି<u>ଁ</u>ର୍ବୁ . ∻ qq 8 8 δ<sub>0</sub> qq qq \_8\_.∕\$ පි රි දේ କୁ 8 9  $\delta$ q  $\delta$  $\delta$ \_\_\_\_

ž ĥ 1253 1254 AGAAAGCCTCAGACAGTAAGGGC-TTTTTTAAAAGAATAAAATGACTTGGCTTTGCGCTTG 1312 1432 1492 1313 GAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTC 1372 CTTCCTGTTCCTGGGGGACCCGCTGGGGCCTTTGGTCTGCATCCCCTGGGCCAGGTCCCTCAG 1552 GGTTGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGCAGCTGGCCTGGCCAGCT 1612 CACACTCTTGTCCTGGGAGGGGGGGGGCCTGATCTCCACCTCGCCTAGTACCTTGGGGACTG 1672 1673 AGGACCTTTTTGGCTTCTTCGCAGCCTGCAAGCCTCTTCCCATGTGTCCCAGCTGCTGTTCC 1732 PAT 2.6-0CT-2001 403 williams.L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Sudduth-Kiinger,J., Reinhard,C., He,Z., Randazzo,F., Kennedy,G.C., Sudduth-Kissam,A., Lamson,G., Dranac,R., Crkvenjakov,R., Dickson,M., Dranac,S., Labat,L., Leshkowitz,D., Kita,D., Garcia,V., Jones,L.W. and Stache-Crain,B. Patent: W0 0172781-A 176 04-0CT-2001; Chiron Corporation (US) Location/Qualifiers 44 AAAAGTCTGCTGACTACTCAGCCAGACCTCCATTACCTCCATCCTGTTGGATTATTTAA 103 163 223 283 343 464 CACACTCTTGTCCTG0GGGGGGGGGGGCAGCTGATCTCACCTCGCCTGGGGACTG 523 583 Euteleostomi; 1194 AAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCTGTTGGATTATTTAA 104 AGAAAGCCTCAGACAGTAAGGGCTTTTTTTTAAAAGAATAAAATGACTTGGCTTG 1433 AGAGTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTGTTGCCGCCTG 14 CTTCCTGTTCCTGGGGGACCCCCTGGGCCTTTGGTCTGCCTGGCCTGGCCAGGTCCCCTGG 164 GAAGGGGGAAGCATTCAGATGAGGGGTTTCTGCATTAACCCTGCCTATCAGGCATCTC GTGTCCTGTGTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGC 524 AGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTNCAGCTGCTGCTCC Gaps Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Butelt Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1; Length 611; 2; Indels linear Score 554; DB 6; 1 Pred. No. 1.4e-126; 0; Mismatches 2; DNA /mol\_type="unassigned DNA" /db\_xref="taxon:9606" TGCTACAAAGGGGGACTGCTCACAGTGGC 1760 /organism="Homo sapiens" /mol\_type="unassigned DNA" /db\_xref="taxon:9606" 611 584 TGCTACAAAGGGGGACTGCTCACAGTGGC AX262096.1 GI:16511048 20.1%; 99.5%; Homo sapiens (human) Query Match 20.1 Best Local Similarity 99.5 Matches 565, Conservative 395 Homo sapiens 1373 1613 1493 1553 1733 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM source RESULT 10 AX262096 LOCUS REFERENCE AUTHORS JOURNAL FEATURES ORIGIN å  $\delta$ qq PP DP  $\delta$  $\delta$ g 8 qq 8 q  $\mathcal{S}$ qq đ 90 3 20 3 g  $\delta$ 

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AmpliTaq Gold Folymerase: 0.07 units/ul Total Vol: 5 ul Buffer: 50 mM MgCl2: 2.5 mM XCl: 50 mM XCl: 50 mM XCl: 50 mM Tris-HCl: 10 mM PH: 8.3 Prepared with primer pairs derived from W86076 Unigene. Prepared with primer pairs derived from W86076 Unigene. Prise action/Qualifiers 1406 Admark from capiens" Admark fraction/Qualifiers 1406 Admark fraction/Qualifiers 1400 Admark fraction/Qua	Query Match9.5%Score 261.2DB 11Length 406Best Local Similarity89.2%Fred. No. 1.1e-53Matches 31Indels 9Gaps 6Matches 347Conservative 0Mismatches 31Indels 9Gaps 6Cov630TTTCTCGTCTCTGTGCGGGCGGGCGGGGGGGGGGGGGG	RESULT 12 AX535063/c LOCUS LOCUS DEFINITION Sequence 90 from Patent W002068633. DEFINITION SCESSION VERSION X5355063.1 GI:25261733 X62TWORDS X5355063.1 GI:25261733 X62TWORDS X5355063.1 GI:25261733 X62TWORDS X5355063.1 GI:25261733 X62TWORDS X5355063.1 GI:25261733 X62TWORDS X5355063.1 GI:25261733 X62TWARDS X632000 AX535063.1 GI:25261733 X62TWARDS X632000 AX535063.1 GI:25261733 X6370700 Saptens (human) X535063.1 GI:25261733 X6370713 X6370700 Saptens (human) X6370703 X637070 X77070 X770700 X77070 X77070 X77070 X770700 X770700 X770700 X770700 X770700 X770700 X770700 X770700 X770700 X770700 X770700 X7707000 X77000000 X7707000 X77070000 X770700000000
ORIGINQuery Match13.0%; Score 357.4; DB 6; Length 395;Duery Match13.0%; Score 357.4; DB 6; Length 395;Best Local Similarity96.9%; Pred. No. 1.2e-77;Matches375; Conservative0; MismatchesQy1216CanacorcarractoractorandaraQy1216C-THTTTPAAGAATGATTATTTPAAGAAAGACTAGACAGTAAGGGQy1276C-THTTTPAAGAATGAATGACTGGATTATTTAAAGAAAGACTAGAGATAAGGGQy1276C-THTTTPAAGAATGAATGACTGGATTATTTAAAGAAAGACTAGAGATAAGGGQy1276C-THTTTPAAGAATGAATGACTGGATTATTTAAAGAAGCACAGAAGAAGAGAGGGGGGAAGGAA	Qy1455GGGAAATGCAGAGCCCTTTGCTTTCTTTGCCGCCTCTTTGCGGGGGACCCGC1511Db249GGGAATGCAGAGCCCTTTGCTTTCCTTTGCTGCCTGGTGGGGGACCGGC308Qy1515TGGGCCTTTGGTCTGCCTGGCCAGGGTCGATGGGGGTGAAGGAGCCGGG309TGGGCCTTTGGTCTGCATCGCCTGGCCAGGGTCGATGGGCTGATGGGGCTGAAGGAGCCGGG309TGGGCCTTTGGTCGGCCAGGCCCTGGGGGTGATGGGCTGATGGGGCTGAAGGAGCCGGGQy1575TTCAAGCAGTGGCAGGCAGGGCGCGGCCAGGGCCAGGGCTGATGGGGCTGAAGGAGCT369Qy1575TTCAAGCAGTGGCAGGCAGGGCGGCCAGGGCCCCCCAGGGCTGATGGGGCGGGGGGGG	Stanford University School of Medicine Department of Genetics, M-344, Stanford, CA 94305, USA Tel: 415729689 Email: myers@shgc.stanford.edu Primer A: AGGTGAAGGCAGTCACA Primer B: GGGGAAGTTTTCAGGCATTCAC STS size: 102 PCR Profile: Thitial incubation: 95 degrees C for 10 minutes PCR Profile: PCR Profile: Denaturation: 94 degrees C for 30 seconds Annealing: 60 degrees C for 30 seconds PCR Vorles: PCR Vorles: PCR Cyrer: Perkin Elmer 9700 Protocol:

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okigin Okigin Okigin Best Local Best Local Best Local Db 238 Oy 238 Oy 256 Oy 256 Oy 256 Db 13 Coression Nbb 13 Coression Nbb 13 Coression Nbb 13 Coression Nbb 13 Coression Nbb 25 Coression Nbb 13 Coression Nbb 13 Coression Nbb 25 Coression Nbb 13 Coression Nbb 25 Coression Nbb 25 Coression Nbb 13 Coression Nbb 25 Coression Nbb
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b Direct Submission Direct Submission of Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 20, 2002 this sequence version replaced gi:23269326. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contrig-scaffold'). Within each contrig-caffold' individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contig scaffold in the feature by sized gaps filled with Ns to the estimated size. The sequence contig scaffold that consist entirely of whole genome shotgun sequence rands of the clone and there may be sequence optim sequence contigs will be indicated in the feature denome shotgun sequence will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature denome shotgun sequence only contigs will be indicated in the feature of the seture of th Pasternak,S., Paul,H., Perez,A., Perez,L., Pfamnkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L. Puazo,M., Quiroz,J., Rachlin,E., Reves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,T., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rous,M., Rose,M., Richards,S., Shen,H., Sanders,W., Savery'G., Scherer,S., Scott,G., Shataman,S., Shen,H., ShettyJ., Shvartsbyn,A., Sisson,I., Sitter,C.D., Smajs,D., ShettyJ., Shvartsbyn,A., Sisson,I., Sitter,C.D., Smajs,D., Shetth,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., UsanaI,K., Valas,R., Vera,V., Villasana,D., Waideon,L., Walke,F., Williams,G., Waiten,R., Wei,K., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Zakub,S., Yen,J., Yoon,L., Yoon,V., Nieferhausern,A., Muss,R., Smith,D.R., Niete,F., Nieferhausern,A., Sheis,R., Smith,D.R., Nies,R., Shun,D., Von Nieferhausern,A., Waiss,R., Smith,D.R., Niete,F., Nieferhausern,A., Sheis,R.A., Neinstrok,G., and Gibbs,R.A. data.html). Direct Submission Submitted (23-SEP-2002) Human Genome Sequencing Center, Department Submitted (23-SEP-2002) Human Genome Sequencing Center, Department Baylor Plaza, Hueston, TX 77030, USA 3 (bases 1 to 190379) Rat Genome Sequencing Consortium. Quality coverage: 5x in Q20 bases; sum-of-contigs estimation NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.h
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the places
is not known and their order in this sequence record is Assembly program: Phrap; version 0.990329 Assembly program: Phrap; version 0.990329 Consensus quality: 168342 bases at least 240 Consensus quality: 171971 bases at least 230 Consensus quality: 174193 bases at least 230 Estimated insert size: 172482; sum-of-contigs estimation Center: Baylor College of Medicine Center: Baylor College of Medicine Center code: Bhtp://www.hgsc.bom.tmc.edu/ Web site: hgsc-help@bom.tmc.edu Project Information Center project name: KCCX Center clone name: CH230-298J1 2 (bases 1 to 190379) Rat Genome Sequencing Consortium. Direct Submission Unpublished table. TITLE JOURNAL REFERENCE REFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL AUTHORS

COMMENT

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will as soon as I

14191: contig of 14191 bp in length 14291: gap of unknown length 190379: contig of 176088 bp in length. 14192 14292 REFERENCE AUTHORS

FEATURES Location/Qualifiers 1. 190379 source / organism="Rattus norvegicus" /mol_types="genomic DNA" /db_tref="taxon:10116"	 N
sc_featur sc_featur	
misc_feature 1271214191 /note="wgs_contig" misc_feature 113270115130	
_ sc_feature	
site: end_sequence:BZ129373" misc_feature 18633188023 /note="wgs_end_extension misc_feature 189275_19379	
_ /note="wgs_end_extension clone_end:Sp6" ORIGIN	 
Query Match 3.2%; Score 87.6; DB 2; Length 190379; Best Local Similarity 65.6%; Pred. No. 2.99-10; Matches 269; Conservative 0; Mismatches 99; Indels 42; Gaps 8;	
Qy     2304     CTGCTGGGAAAAGCTTTGCGGGGGCTTGCTTGGTTAACCACAGAAGGAGAAGGGACTGTT     2363       Db     5492     CTGCTGGGGAAGAGCTTAGTGGGGGCTAGTATCAGAGAAGGAAGGAACTGTT     5438	
Qy     2364     GGGGTGCTCTCTGCAGCCTCCCCGTGCTGGGTGGGAGCACGGTTACTGTGTTCTTAAT     2423       Db     5437     CATGCACTGACTTATCTCTTCCTGCTGGGGTAAAGGCTTGGTTACTTTCTTAT     2381	
ATGTAACCTCCACACCTTTCTCCAGATT 248	
5380 GCTTCGAAGTGATTCCTGAGGTTTTCTCACACCTACCTTCTTCTTCCTGGGG 532	
QY     218     030716171717171040101616161616161616161616161616161616	
QY     2544     GTCAGGTGGGGTGAGGCTCCTGGGGGGGGGGGGGGGTGGGGGTTCAAGTTGTCTG     2602       DD     111     1111     1111     1111     1111       DD     5276     GTCAAATGTGTGTAGCGGGTCATGGGGGGGGCCATGGAAACCCAAGTTGTCATAATG     5217	
QY     2603     CCATGTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTTACTGTGCGGA     2662       Db     1	
Qy     2663     CGAGAAGTCTGTATGTGGGATTCGGGTTAGAATGGAATAAAAC     2712       0     1	
RESULT 14 AC136817 LOCUS AC136817 231580 bp DNA linear HTG 23-NOV-2002 DEFINITION Ratus norvegicus clone CH230-43B4, *** SEQUENCING IN PROGRESS ***, DEFINITION Ratus norvegicus clone CH230-43B4, *** SEQUENCING IN PROGRESS ***, ACCESSION AC136817 2 G1:25188334 VERSION AC136817.2 G1:25188334 ATG; HTG; HTGS_PRAFT; HTGS_ENRICHED. Ratus norvegicus (Norway rat) SOURCE Ratus norvegicus (Norway rat) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ratus norvegicus (Nordata; Craniata; Vertebrata; Euteleostomi; Ratus norvegicus Ratus Rodentia; Sciurognathi; Muridae; Murinae; Ratus Norda; Ratus Nodentia; Sciurognathi; Muridae; Murinae;	

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0Y       2424       GTTCATGTATTTAAAATGATTTCTTTCTAAGGTGTAACCTCCACACTTTCTCCCGGATT       2483         0P       225408       GCTTCGAGTTATTAAAATGATTTCTCAGGTTTCTCACACCTTTCTTCCCGGATT       2483         0P       225408       GCTTCGAGTTATTTCTAAAGGTGGTGGGTGGTTGGTCGCCTTGCTCCGGGTG       225459         0P       225460       GGCTGATTTTTCTAAAGGTGGTGGGGGGGGGGGGGGGGG	225616 TGAGAAATCTGTATGTGGGGCCTCTGTGC-TGGGTCAGATGCAATAAAAC 225 SULT 15 225616 TGAGAAATCTGTATGTGGGGCCTCTGCC-TGGGTCAGAATGCAATAAAAC 225 S01DT7 CUS CUS CUS CNS01DT7 FINITION Human chromosome 14 0f Homo sapiens (Human), complete seg AL132642.4 G1:14041778 AL132642.4 G1:14041778 AL120642.4 G1:14041778 AL120642.4 G1:14041778 AL120642.4 G1:14041778 AL120642.4 G1:14041778 AL120642.4 G1:14041778 AL120642.4 G1:140641778 AL120642.4 G1:14041778 AL120642.4 G1:1404178 AL120642.4 G1:1404178 AL120642.4 G1:1404178 AL120642.4 G1:1404178 AL120642.4 G1:1404178 AL120642.4 G1:1404178 AL120642.4 G1:1404178 AL120642.4 G1:1404178 AL120642.4 G1:1404178 AL120642.4 AL120642.4 AL120642.4 AL12064444 AL120642.4 AL1206444478 AL1206444474744747478 AL120644447474747474747474747474747474747474	<pre>JUTLE Sequencing of the numan chromosome re JOURNAL Sequencing of the numan chromosome re AUTHOR Direct Submission TITTLE Direct Submission TITTLE Direct Submission FBP 191 91006 EVEX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Genoscope.cns.fr) TITTLE Direct Submission DOURNAL Submission FBP 191 91006 EVEX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Conversion To May 15, 2001 this sequence version replaced gi:8217878. - Web : www.genoscope.cns.fr Conversion Contact: Sequef@genoscope.cns.fr Contact: Sequef@geno</pre>
contigs within a contig-scaffold that consist entirely of whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence only contigs will be indicated in the feature shorgun sequence only contigs will be indicated in the feature table. 	<pre>public control of a control of a control of cont control of control of control of control of control of c</pre>	<pre>misc_feature 1.1287 misc_feature 1.000e_endi5p6" misc_feature 1.1287 clone_endi5p6" misc_feature 13382653 misc_feature 13382653 misc_feature 13382653 misc_feature 13369156 misc_feature 13375.9 misc_feature 13375. misc_feature 140. misc_feature 140. misc_featu</pre>

з 6767 датбаататттсттттбтттбатбатбабадсаттатстттаадссасааттаббсаааа 36826 36827 тестатсссатадададаттссаттттстсаттастадасстататадататт 36886 36887 GTACTTAGTTATTATGTTTTAAATTTCATCAACAA-TAATAATTTATGGAAATTTGTTCTGTC 36945 37006 ATACTTACTACTTGCTCCCCCTCGCAGAACTAGTACTCGCGCACTCCTCCTCTTTTGATCGCA 37065 1000 CTCCCCCATCACAAAAAAAATTCCTTATTTTTAGTAGACATGTATTTTACCAAAAAATAT 1059 1120 TTA--------CGCCAACATAATATTTGATTTTGCCTCTTGGCTCTGAAAGCCCCAAA 1167 1168 ATATTTACCGTCTAGCCCGTTACAGAAAAGTCTGCTGGTACTACTGAGCCAGACCTCCATT 1227 1228 ACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGGCCTTTTTTAAAAG 1287 2 940 GCTGTTTATGCCACTGATTTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTT 999 Query Match 2.9%; Score 81; DB 9; Length 182643; Best Local Similarity 54.5%; Pred. No. 1.3e-08; Matches 213; Conservative 0; Mismatches 165; Indels 13; Gaps Identified using the e-PCR software (G. Schuler)" 157650. 157856 /note="matching EMBL:T03336 RHdD:rH53909 dbSTS:STS67159 dbSTS:STS67159 167011: 1670886 /note="matching EMBL:AA195225 FHdb:RF65774 dbSTS:STS45705 dbSTS:STS45705 dbSTS:STS45705 dbSTS:STS45705 dbSTS:STS45705 dbSTS:STS45705 dbSTS:STS45705 dbSTS:STS454705 dbSTS:STS444705 dbSTS:STS454705 dbSTS+205 Identified using the e-PCR software (G. Schuler)" Percentage of bases with a quality value >= 40 : 99 %. /organism="Homo sapiens" /db\_trefs="texon:9606" /db\_trefs="texon:9606" /chromosome="14" /clone="14" /clone="1 37126 CTGGAAAGGCCCTCGGAGGTCTTCTAAACCA 37156 162845. .162997 /note="matching EMBL:AA610019 RHdb:RH94166 1288 AATAAAATGACTTGGTTTGCGCTTGGAAGCA 1318 Search completed: November 29, 2004, 11:55:34 Job time : 11599 secs ocation/Qualifiers 1. .182643 80 - 89 : 59044 90 - 99 : 101315 source STS STS STS STS FEATURES ORIGIN qq q  $\mathcal{S}$ q  $\delta$ qq  $\mathcal{S}$ g  $\delta$ Q0  $\mathcal{S}$ q 8  $\mathcal{S}$ 

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